

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 20, 2005, 11:04:48 ; Search time 161 Seconds
(without alignments)
153.007 Million cell updates/sec

Title: US-09-826-791A-2

Perfect score: 1712

Sequence: 1 MEPNGTFSNNRNCTIENF.....KAKTKCVFVSWLRKETRV 330

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued P Genes AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1703	69.5	346	4	US-09-585-876-2
2	559	32.7	337	3	US-09-044-404A-2
3	559	32.7	337	4	US-09-586-924-2
4	479	28.0	339	1	US-08-153-848-44
5	479	28.0	339	2	US-08-812-871-3
6	479	28.0	339	3	US-09-299-843A-44
7	479	28.0	339	3	US-09-088-337B-44
8	479	28.0	339	4	US-09-170-496D-32
9	479	28.0	339	5	PCT-US93-11153-44
10	479	28.0	339	5	PCT-US95-07180-2
11	476	27.8	339	4	US-09-170-496D-182
12	461	26.9	362	3	US-08-513-974B-374
13	445	26.1	373	4	US-09-745-842-14
14	442	25.8	373	2	US-08-559-524A-4
15	442	25.8	373	3	US-08-749-707-4
16	442	25.8	373	4	US-09-947-922-4
17	440	25.7	361	1	US-08-383-750-4
18	440	25.7	361	3	US-08-352-678-4
19	440	25.7	361	4	US-09-536-954-4
20	440	25.7	361	4	US-09-170-496D-78
21	440	25.7	361	4	US-09-929-583B-4
22	440	25.7	361	5	PCT-US93-09636-4
23	439.5	25.7	348	3	US-08-852-824-17
24	439	25.6	302	2	US-08-467-948A-30
25	439	25.6	302	3	US-08-467-947A-30
26	437	25.5	344	2	US-08-467-948A-8
27	437	25.5	344	3	US-08-467-947A-8

28	434	25.4	361	4	US-09-170-496D-206	Sequence 206, Appl
29	434	25.4	377	4	US-09-745-842-17	Sequence 17, Appl
30	430	25.1	370	3	US-08-781-250-2	Sequence 2, Appl
31	424.5	24.8	374	4	US-09-745-842-15	Sequence 15, Appl
32	419.5	24.5	374	4	US-09-102-710B-3	Sequence 3, Appl
33	416.5	24.3	373	3	US-08-513-974B-373	Sequence 373, Appl
34	416	24.3	342	3	US-08-988-876-9	Sequence 9, Appl
35	416	24.3	375	1	US-08-442-134A-2	Sequence 2, Appl
36	416	24.3	375	1	US-08-446-088A-2	Sequence 2, Appl
37	416	24.3	375	2	US-08-559-524A-3	Sequence 3, Appl
38	416	24.3	375	3	US-08-749-707-3	Sequence 3, Appl
39	416	24.3	375	4	US-09-947-922-3	Sequence 3, Appl
40	409.5	23.9	342	4	US-09-054-272-2	Sequence 2, Appl
41	406.5	23.7	398	1	US-08-097-938-6	Sequence 6, Appl
42	406.5	23.7	398	1	US-08-476-000-6	Sequence 6, Appl
43	406.5	23.7	398	1	US-08-472-840-6	Sequence 6, Appl
44	406.5	23.7	398	2	US-08-476-976-6	Sequence 6, Appl
45	406.5	23.7	398	2	US-08-476-976-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-585-876-2
; Sequence 2, Application US/09585876
; Patent No. 6586205
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: 43239, A NO. 6586205el GPCR-Like Molecule and
; FILE REFERENCE: 5800-88
; CURRENT APPLICATION NUMBER: US/09/585,876
; CURRENT FILING DATE: 2000-06-01
; EARLIER APPLICATION NUMBER: 60/182,061
; EARLIER FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-585-876-2

Query Match		99.5%	Score 1703;	DB 4;	Length 346;
Best Local Similarity		99.4%	Pred No 3.7e-124;		
Matches 328;		Conservative 1;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	MEPNGTFSNNRNCTIENF	KREFFFPIVYLIIFFWGLGNGLSIYVFLQPKKSTSVNVF	60	
Db	17	MEPNGTFSNNRNCTIENF	KREFFFPIVYLIIFFWGLGNGLSIYVFLQPKKSTSVNVF	76	
Qy	61	MLNLAI	SDLLFIETLPRADYILRGNSWIFGDLACRIMSLSLYNMYSIYFLTVLSVR	120	
Db	77	MLNLAI	SDLLFIETLPRADYILRGNSWIFGDLACRIMSLSLYNMYSIYFLTVLSVR	136	
Qy	121	FLANVHPFRLHVT	SIRSAWILCGIITWILIMASSIMLLDSGSEONGSVTSCLELNLYKIA	180	
Db	137	FLANVHPFRLHVT	SIRSAWILCGIITWILIMASSIMLLDSGSEONGSVTSCLELNLYKIA	196	
Qy	181	KLQTMNYIALVWGCLLP	FFFTLSICYLLIIRVLKVEVPESGLRVSHRKALTTIITLIIF	240	
Db	197	KLQTMNYIALVWGCLLP	FFFTLSICYLLIIRVLKVEVPESGLRVSHRKALTTIITLIIF	256	
Qy	241	FLCFLPYHTLRTVH	LTTWKVGLCKDLHKLAVITLALAAANACFNPLLYFAGENFKDRL	300	
Db	257	FLCFLPYHTLRTVH	LTTWKVGLCKDLHKLAVITLALAAANACFNPLLYFAGENFKDRL	316	
Qy	301	KSALRKGHPOKAKT	KCVFVSWLRKETRV	330	
Db	317	KSALRKGHPOKAKT	KCVFVSWLRKETRV	346	

QY	302	SALRK	306
Db	307	STFRK	311
RESULT 3			
US-09-586-924-2			
; Sequence 2, Application US/09586924			
; Patent No. 6506878			
; GENERAL INFORMATION:			
; APPLICANT: SATHE, GANESH M.			
; APPLICANT: HALSEY, WENDY			
; APPLICANT: ELLIS, CATHERINE E.			
; APPLICANT: AMES, ROBERT S.			
; APPLICANT: FOLEY, JAMES J.			
; APPLICANT: SARAU, HENRY M.			
; APPLICANT: CHAMBERS, JON			
; TITLE OF INVENTION: CDNA CLONE HMTMF81 THAT ENCODES A NOVEL			
; FILE REFERENCE: GH-70001-1D1			
; CURRENT APPLICATION NUMBER: US/09/586.924			
; PRIOR FILING DATE: 2000-06-05			
; PRIOR APPLICATION NUMBER: 09/044,404			
; PRIOR FILING DATE: 1998-03-19			
; PRIOR APPLICATION NUMBER: 08/844,795			
; NUMBER OF SEQ ID NOS: 2			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 2			
; LENGTH: 337			
; TYPE: PRT			
; ORGANISM: HOMO SAPIENS			
US-09-586-924-2			
Query Match 32.7%; Score 559; DB 4; Length 337;			
Best Local Similarity 38.0%; Pred. No. 7.7e-36;			
Matches 116; Conservative 71; Mismatches 106; Indels 12; Gaps 7;			
QY	11	NSRNC--TIENFKREFFPIVYLIIFFWGVNGLSIYVFLOPKKTSVNFMNLAI	SD 68
Db	10	SSATCHDTIDDFRNQVYSTLYSMISVVGFNGFVLVIKTTHKSAFYMINLA	VAD 69
QY	69	LFIPTLPFRADYILRGSNWIFGDLACRIMSYSLVNNMYSIYFLTIVSVRF	FLAMVHPF 128
Db	70	LLCVCTPLRVVYVHKGIWLFGDFCLRLSTYALYNLYCSIFFMTAMSFR	CIAIVFPV 129
QY	129	RLHVTISRASWILCGIWI-LIMASSIMLDSSEQSGSVTSCLELNLYKIAK-	-LQTM 185
Db	130	QNINLVTKARFCVCGIWFIVLTSSPFLMAKPQKGKNKTCFEPPQDNQT	KNHVLVL 189
QY	186	NVALVWGCLPFPTLSICYLLIRVLKVVEPSGLRVSHRKALTITITLIIF	FLCFL 245
Db	190	HVSFLVGFIIPFVIIVCYTMIILTLLKKSKNKN--LSSHKAIGMIMVTA	AFLVSFM 247
QY	246	PYHTLTRVHLTTW--KVGCLKD--RLHKALVITLALAANAACFNPLYFA	GENDKDRLK 301
Db	248	PHIQORTLHLHFHLHNETHPCDSVLRMQKSVMITLSAANSNCCFDPPLL	YFFSGGNFRKL- 306
QY	302	SALRK	306
Db	307	STFRK	311
RESULT 4			
US-08-153-848-44			
; Sequence 44, Application US/08153848			
; Patent No. 5759804			
; GENERAL INFORMATION:			
; APPLICANT: Godiska, Ronald			
; APPLICANT: Gray, Patrick W.			
; APPLICANT: Schwaikart, Vicki L.			

; TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors

; NUMBER OF SEQUENCES: 64

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

; ADDRESSEE: Bicknell,

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/153,848

; FILING DATE:

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/977,452

; FILING DATE: 17-NOV-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 5759804e1, Greta E.

; REGISTRATION NUMBER: 35,302

; REFERENCE/DOCKET NUMBER: 31794

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 474-6300

; TELEFAX: (312) 474-0448

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 44:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 339 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-153-848-44

Query Match 28.0%; Score 479; DB 1; Length 339;

Best Local Similarity 34.8%; Pred. No. 1.2e-29;

Matches 112; Conservative 62; Mismatches 126; Indels 22; Gaps 9;

QY 7 FSNNSRNCCTIEN-FKREFPPIVYLIIFFGVLGNGLSIYVFLQPYKYSTVNVFMLNLA 65

Db 15 FSLATBQCQCQETPLENMLFASFYLLDFILALVGNLTALWLFIRDHKSCTPANVFLMHLA 74

QY 66 ISDLLFISTLPFRADYVYLRGNSWIFGDLACRIMSISLYVNMYSIYFLTVLSVVRFLAMV 125

Db 75 VADLSCVLVLPTRLVYVHFGSNHWPFGIEACRLTGFLFYLNMYSIYFLTICISADRFPLAIV 134

QY 126 HPFRLHVTISRANILCGIWIILI-MASSIMLLDSGSEQSVTSCLNLYKIAKLQT 184

Db 135 HPVKSLKLRPLAHLACAFWVAVAMAPLLVSPQTQNTHTVVCLQ--LYR-EKASH 191

QY 185 MNYIALVVGCLLPFFTLSCYLLIIRVLLKVEPESGLRVSHR---KALTTIITLIIF 241

Db 192 HALVSLAVAFPTFFITVTTCYLLIIRSL-----ROGLRVEKRLKTKAVRMIAIVLAIFL 245

QY 242 LCFPLPHTLTTHVLTWKV--GLCKDRLHKALV--ITLALAAANACFNPLLYFAGENFK 297

Db 246 VCFVPYVHNRSVYVLYHRSHGASCATORILANRITSCITSLNGALDPIIMYFFVAEKFR 305

QY 298 DRLSAL----RKGHPOKAKTK 315

Db 306 HALCNLLCGKRLKGPSPSPGK 327

RESULT 5

US-08-812-871-3

; Sequence 3; Application US/08812871

; Patent No. 5953303

; GENERAL INFORMATION:

; APPLICANT: Au-Young, Janice

; APPLICANT: Guegler, Karl

; APPLICANT: Muzong Cheng

; TITLE OF INVENTION: NOVEL HUMAN CHEMOKINE RECEPTOR-LIKE

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Dr.

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/812,871

; FILING DATE: Filed Herewith

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0237 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 339 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; IMMEDIATE SOURCE:

; LIBRARY: GenBank

; CLONE: 992700

US-08-812-871-3

Query Match 28.0%; Score 479; DB 2; Length 339;

Best Local Similarity 34.8%; Pred. No. 1.2e-29;

Matches 112; Conservative 62; Mismatches 126; Indels 22; Gaps 9;

QY 7 FSNNSRNCCTIEN-FKREFPPIVYLIIFFGVLGNGLSIYVFLQPYKYSTVNVFMLNLA 65

Db 15 FSLATBQCQCQETPLENMLFASFYLLDFILALVGNLTALWLFIRDHKSCTPANVFLMHLA 74

QY 66 ISDLLFISTLPFRADYVYLRGNSWIFGDLACRIMSISLYVNMYSIYFLTVLSVVRFLAMV 125

Db 75 VADLSCVLVLPTRLVYVHFGSNHWPFGIEACRLTGFLFYLNMYSIYFLTICISADRFPLAIV 134

QY 126 HPFRLHVTISRANILCGIWIILI-MASSIMLLDSGSEQSVTSCLNLYKIAKLQT 184

Db 135 HPVKSLKLRPLAHLACAFWVAVAMAPLLVSPQTQNTHTVVCLQ--LYR-EKASH 191

QY 185 MNYIALVVGCLLPFFTLSCYLLIIRVLLKVEPESGLRVSHR---KALTTIITLIIF 241

Db 192 HALVSLAVAFPTFFITVTTCYLLIIRSL-----ROGLRVEKRLKTKAVRMIAIVLAIFL 245

QY 242 LCFPLPHTLTTHVLTWKV--GLCKDRLHKALV--ITLALAAANACFNPLLYFAGENFK 297

Db 246 VCFVPYVHNRSVYVLYHRSHGASCATORILANRITSCITSLNGALDPIIMYFFVAEKFR 305

QY 298 DRLSAL----RKGHPOKAKTK 315

Db 306 HALCNLLCGKRLKGPSPSPGK 327

RESULT 6

US-09-299-843A-44

; Sequence 44, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-299-843A-44

Query Match 28.0%; Score 479; DB 3; Length 339;
Best Local Similarity 34.8%; Pred. No. 1.2e-29;
Matches 112; Conservative 62; Mismatches 126; Indels 22; Gaps 9;
QY 7 FSNNSRNTCTIEN-FKREFFPIVYLIIFFWGLNGLSIYVFLQPKYKSTSVNFMNLIA 65
DB 15 FSLATAEQCGQTPIENMLFASFYLLDFILALVGNLTALWLFIRDKSGTTPANVFLMHLA 74
QY 66 ISDLLFIETLPPRADIYLRGNSWIFGDLACRIMSYSLYVNMYSIYFVLTVLSVVRFLAMV 125
DB 75 VADLSVCLVLPTRLVYHFSGNHWPFGEIACRLTGFLFYLNMYASIVFVLTICISADRLAIV 134
QY 126 HPFRLHVTISRAMLGIIWILI-MASSIMLLDSGSEONGSVTSCLELNLYKIAKLOT 184
DB 135 HPVKSLKLRRLPYLAHLACAFLLWVAVAMAPLLVSPQTQVTHVTVCLO--LYR-EKASH 191
QY 185 MNVIALVGCGLPFFTLSTCYLLIIRVLLKVEPESGLRVSHR---KALTITIIITLIIPF 241
DB 192 HALVSLAVAFTEFFITVTTCYLLIIRSL-----RQGLRVERKLTQKAVMTAIVLAIFL 245
QY 242 LCFPLPYHLRTVHLTTWKV--GLCKDRHLKALV--ITLALAAANACFNPLLYFAGENFK 297
DB 246 VCFVPYHNRSVVVLHYRSHGASCATORILANRITSCLTSLINGALDPIMYFFVFAEKFR 305

QY 298 DRLKSAL----RKGHPOKAKTK 315
DB 306 HALCNLLCGRLKRGPPSPPEKG 327
RESULT 7
US-09-088-337B-44
; Sequence 44, Application US/09088337B
; Patent No. 6348574
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; Gray, Patrick W.
; Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/088,337B
; FILING DATE: 01-JUN-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6348574and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-088-337B-44

Query Match 28.0%; Score 479; DB 3; Length 339;
Best Local Similarity 34.8%; Pred. No. 1.2e-29;
Matches 112; Conservative 62; Mismatches 126; Indels 22; Gaps 9;
QY 7 FSNNSRNTCTIEN-FKREFFPIVYLIIFFWGLNGLSIYVFLQPKYKSTSVNFMNLIA 65
DB 15 FSLATAEQCGQTPIENMLFASFYLLDFILALVGNLTALWLFIRDKSGTTPANVFLMHLA 74
QY 66 ISDLLFIETLPPRADIYLRGNSWIFGDLACRIMSYSLYVNMYSIYFVLTVLSVVRFLAMV 125
DB 75 VADLSVCLVLPTRLVYHFSGNHWPFGEIACRLTGFLFYLNMYASIVFVLTICISADRLAIV 134
QY 126 HPFRLHVTISRAMLGIIWILI-MASSIMLLDSGSEONGSVTSCLELNLYKIAKLOT 184
DB 135 HPVKSLKLRRLPYLAHLACAFLLWVAVAMAPLLVSPQTQVTHVTVCLO--LYR-EKASH 191
QY 185 MNVIALVGCGLPFFTLSTCYLLIIRVLLKVEPESGLRVSHR---KALTITIIITLIIPF 241

Db 192 HALVSLAVAFPPFTTTCVLLIIRSL-----RQGLRVKRLKTKAVRMIAIVLAIFL 245
Qy 242 LCFPLVHTLRTVHLTTWKV--GLCKDLRLHKALV--ITLALAAANACFNPLLYFAGENFK 297
Db 246 VCFVPYHVNRSVVYLHYRSHGASCATORILANRITSCLTSLNGALDPIPIYFFVAEKR 305
Qy 298 DRLKSAL-----RKGHPOKAKTK 315
Db 306 HALCNLLCGKRLKGPPSPFEGK 327

RESULT 8
US-09-170-496D-32
; Sequence 32, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 32
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-32

Query Match 28.0%; Score 479; DB 4; Length 339;
Best Local Similarity 34.8%; Pred. No. 1.2e-29;
Matches 112; Conservative 62; Mismatches 126; Indels 22; Gaps 9;

Qy 7 FSNNSNRCTIEN-FKREFFPIVYLIIFFWGVNLGLSIYVFLQPYKKSTSVNVFMLNLA 65
Db 15 FSLATAEQCGQETPLENMLFASFYLLDFILALVGNLTALMLFIRDHKSGETPANVFLMHLA 74
Qy 66 ISDLLFTSTLPPRADYLRGNSWIFGLDACHIMSYSLVNMYSIYELTVLSVVREFLAMV 125
Db 75 VADUSCVLVLPLRLVYHFGSNHWPFGIACRLTGLFYLNNYASIFLTCISADRFLEAIV 134
Qy 126 HPFRLHVTIRSRAWILCGIWIILI-MASSIMLDSDGSEQNGSVTSCLEMLNYKIAKLQT 184
Db 135 HPVSKLRLRPLRYAHLACAFLLVAVAMAPLLVSPQVTQNTHTVVCLO--LYR-EXASH 191
Qy 185 MNYIALVVGCLLPFTLSICYLLIIRVLLKVEVPESGLRVSHR---KALTTIITLIIFP 241
Db 192 HALVSLAVAFPPFTTTCVLLIIRSL-----RQGLRVKRLKTKAVRMIAIVLAIFL 245
Qy 242 LCFPLVHTLRTVHLTTWKV--GLCKDLRLHKALV--ITLALAAANACFNPLLYFAGENFK 297
Db 246 VCFVPYHVNRSVVYLHYRSHGASCATORILANRITSCLTSLNGALDPIPIYFFVAEKR 305
Qy 298 DRLKSAL-----RKGHPOKAKTK 315
Db 306 HALCNLLCGKRLKGPPSPFEGK 327

RESULT 9
PCT-US93-11153-44
; Sequence 44, Application PC/TUS9311153
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell

; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11153
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-11153-44

Query Match 28.0%; Score 479; DB 5; Length 339;
Best Local Similarity 34.8%; Pred. No. 1.2e-29;
Matches 112; Conservative 62; Mismatches 126; Indels 22; Gaps 9;

Qy 7 FSNNSNRCTIEN-FKREFFPIVYLIIFFWGVNLGLSIYVFLQPYKKSTSVNVFMLNLA 65
Db 15 FSLATAEQCGQETPLENMLFASFYLLDFILALVGNLTALMLFIRDHKSGETPANVFLMHLA 74
Qy 66 ISDLLFTSTLPPRADYLRGNSWIFGLDACHIMSYSLVNMYSIYELTVLSVVREFLAMV 125
Db 75 VADUSCVLVLPLRLVYHFGSNHWPFGIACRLTGLFYLNNYASIFLTCISADRFLEAIV 134
Qy 126 HPFRLHVTIRSRAWILCGIWIILI-MASSIMLDSDGSEQNGSVTSCLEMLNYKIAKLQT 184
Db 135 HPVSKLRLRPLRYAHLACAFLLVAVAMAPLLVSPQVTQNTHTVVCLO--LYR-EXASH 191
Qy 185 MNYIALVVGCLLPFTLSICYLLIIRVLLKVEVPESGLRVSHR---KALTTIITLIIFP 241
Db 192 HALVSLAVAFPPFTTTCVLLIIRSL-----RQGLRVKRLKTKAVRMIAIVLAIFL 245
Qy 242 LCFPLVHTLRTVHLTTWKV--GLCKDLRLHKALV--ITLALAAANACFNPLLYFAGENFK 297
Db 246 VCFVPYHVNRSVVYLHYRSHGASCATORILANRITSCLTSLNGALDPIPIYFFVAEKR 305
Qy 298 DRLKSAL-----RKGHPOKAKTK 315
Db 306 HALCNLLCGKRLKGPPSPFEGK 327

RESULT 10
PCT-US95-07180-2
; Sequence 2, Application PC/TUS9507180
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: GOCAYNE, JEANINE D
; APPLICANT: RUBEN, STEVEN M
; TITLE OF INVENTION: G-PROTEIN RECEPTOR HIBEB69
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,

```
; ADDRESSEE: STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NJ
; COUNTRY: US
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07180
; FILING DATE: 06-JUNE-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 30,073
; REFERENCE/DOCKET NUMBER: 325800-366
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-07180-2

Query Match      28.0%; Score 479; DB 5; Length 339;
Best Local Similarity 34.8%; Pred. No. 1.2e-29;
Matches 112; Conservative 62; Mismatches 126; Indels 22; Gaps 9;

QY  7 FSNNSNRNCTIEN-FKREFFPIVYLIIFFMGVLNGLSIYVFLQPYKKSTSVNVFMLNLA 65
Db  15 FSLATAEQCGQETPLENMLFASFYLLDFILALVGNLTALWLFIRDHKSGETPANVFLMHLA 74
QY  66 ISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSIYFLTVLSVVRFLAMV 125
Db  75 VADLSCVLVPTRLVYHFGSNHWPFGIEACRLTGFLFYLNMVYASIFLTCISADRELAIV 134
QY  126 HPRLHLVTSIRSAILCGIITWLI-MASSIMLLDSGSEONGSVTSCLEINLYKIAKLQT 184
Db  135 HPVKSILKRLRPLYAHLACAFWVAVAMAPLVSPQTQVNTHTVVCLQ--LYR-EKASH 191
QY  185 MNVIALVWGCLLPFTLSICYLLIIIRVLLKVEVPESGLRVSHR---KALTTIITLIIFP 241
Db  192 HALVSLAVAFPTFTTVCYLLIIIRSL-----RQGLRVEKRLTKAVRMIAIVLAIFL 245
QY  242 LCPFLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACFNPLLYFAGENFK 297
Db  246 VCFVPYHVNRSVYLVHYRSHGASCATQRIALANRITSLTSLNGALDPMYFFVAEKFR 305
QY  298 DRLLKSAL----RKGHPQKAKTK 315
Db  306 HALCNLLCGKRLKGPSPPEGK 327

RESULT 11
US-09-170-496D-182
; Sequence 182, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 182
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-182

Query Match      27.8%; Score 476; DB 4; Length 339;
Best Local Similarity 34.8%; Pred. No. 2e-29;
Matches 112; Conservative 61; Mismatches 127; Indels 22; Gaps 9;

QY  7 FSNNSNRNCTIEN-FKREFFPIVYLIIFFMGVLNGLSIYVFLQPYKKSTSVNVFMLNLA 65
Db  15 FSLATAEQCGQETPLENMLFASFYLLDFILALVGNLTALWLFIRDHKSGETPANVFLMHLA 74
QY  66 ISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSIYFLTVLSVVRFLAMV 125
Db  75 VADLSCVLVPTRLVYHFGSNHWPFGIEACRLTGFLFYLNMVYASIFLTCISADRELAIV 134
QY  126 HPRLHLVTSIRSAILCGIITWLI-MASSIMLLDSGSEONGSVTSCLEINLYKIAKLQT 184
Db  135 HPVKSILKRLRPLYAHLACAFWVAVAMAPLVSPQTQVNTHTVVCLQ--LYR-EKASH 191
QY  185 MNVIALVWGCLLPFTLSICYLLIIIRVLLKVEVPESGLRVSHR---KALTTIITLIIFP 241
Db  192 HALVSLAVAFPTFTTVCYLLIIIRSL-----RQGLRVEKRLTKAVRMIAIVLAIFL 245
QY  242 LCPFLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACFNPLLYFAGENFK 297
Db  246 VCFVPYHVNRSVYLVHYRSHGASCATQRIALANRITSLTSLNGALDPMYFFVAEKFR 305
QY  298 DRLLKSAL----RKGHPQKAKTK 315
Db  306 HALCNLLCGKRLKGPSPPEGK 327

RESULT 12
US-08-513-974B-374
; Sequence 374, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Onaka, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ogi, Kazuhiro
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995
; PRIOR APPLICATION DATA:
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RESULT 13
US-09-745

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 20, 2005, 07:35:07 ; Search time 960 Seconds
(without alignments)
176.027 Million cell updates/sec

Title: US-09-826-791a-2

Perfect score: 1712

Sequence: 1 MEPNGTFSNNRNCTIENF.....KAKTKCFVSVWLKRETRV 330

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1712	100.0	346	1 CLT2_HUMAN	Q9ns75 homo sapien
2	1367.5	79.9	345	1 CLT2_PIG	Q95n03 sus scrofa
3	1204	70.3	309	2 Q8R528	Q8r528 mus musculus
4	1197	69.9	309	1 CLT2_MOUSE	Q820a1 mus musculus
5	1187	69.3	309	1 CLT2_RAT	Q824t9 rattus norv
6	567.5	33.1	339	1 CLT1_RAT	Q924t8 rattus norv
7	563	32.9	340	1 CLT1_PIG	Q95n02 sus scrofa
8	560	32.7	352	1 CLT1_MOUSE	Q99ja4 mus musculus
9	559	32.7	337	1 CLT1_HUMAN	Q9y271 homo sapien
10	553	32.3	337	2 Q8IV19	Q8iv19 homo sapien
11	487.5	28.5	337	1 G880_HUMAN	Q96p68 homo sapien
12	479	28.0	337	2 Q6Y1R5	Q9y1r5 rattus norv
13	479	28.0	367	1 G817_HUMAN	Q13304 homo sapien
14	477	27.9	339	2 Q8N5S7	Q8n5s7 homo sapien
15	477	27.9	347	2 Q7ZZA4	Q7zza4 brachydanio
16	473.5	27.7	349	2 Q6P852	Q6p852 xenopus tro
17	470	27.5	362	1 P2YR_MELGA	P49652 melesgria g
18	468	27.3	337	2 Q6Y1F8	Q6y1f8 mus musculus
19	467	27.3	362	1 P2YR_CHICK	P34996 gallus gall
20	459	26.8	339	2 Q6NS65	Q6ns65 mus musculus
21	457	26.7	357	2 Q3DE05	Q3de05 raja erinac
22	456	26.6	249	2 Q6S9C7	Q6s9c7 chinchilla
23	454	26.5	373	1 P2YR_CAVPO	P39902 cavia porce
24	453	26.5	361	2 Q90X57	Q90x57 xenopus lae
25	449.5	26.3	357	2 Q7TMV7	Q7tmv7 mus musculus
26	447	26.1	308	1 P2Y5_CHICK	P32250 gallus gall
27	447	26.1	373	1 P2YR_RAT	P49651 rattus norv
28	446	26.1	373	1 P2YR_HUMAN	P49000 homo sapien
29	442	25.8	373	1 P2YR_BOVIN	P48042 bos taurus
30	442	25.8	373	1 P2YR_MOUSE	P49650 mus musculus
31	440	25.7	361	1 EB12_HUMAN	P32249 homo sapien

RESULT 1

ID	CLT2_HUMAN	STANDARD;	PRT;	346 AA.
AC	Q9NS75; Q9HCQ2;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Cysteinyln leukotriene receptor 2 (CysLTR2) (P5EC0146) (HG57) (HPN321)			
DE	(HGPCR21).			
GN	Name=CysLTR2; Synonyms=CysLT2, CysLT2R;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RX	MEDLINE=20374466; PubMed=10913337; DOI=10.1006/bbrc.2000.3140;			
RA	Takasaki J., Kamohara M., Matsumoto M., Saito T., Sugimoto T., Ota T.,			
RA	Nishikawa T., Kawai Y., Masuho Y., Isogai Y., Suzuki Y., Sugano S.,			
RA	Furuichi K.;			
RT	"The molecular characterization and tissue distribution of the human			
RT	cysteinyln leukotriene CysLT2 receptor.";			
RL	Biochem. Biophys. Res. Commun. 274:316-322(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20459128; PubMed=10851239; DOI=10.1074/jbc.M003490200;			
RA	Heise C.E., O'Dowd B.F., Figueroa D.J., Sawyer N., Nguyen T.,			
RA	Im D.S., Stocco R., Bellefeuille J.N., Abramovitz M., Cheng R.,			
RA	Williams D.L. Jr., Zeng Z., Liu Q., Ma L., Clements M.K., Coulombe N.,			
RA	Liu Y., Austin C.P., George S.R., O'Neill G.P., Metters K.M.,			
RA	Lynch K.R., Evans J.F.;			
RT	"Characterization of the human cysteinyl leukotriene 2 receptor.";			
RL	J. Biol. Chem. 275:30531-30536(2000).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20545741; PubMed=11093801;			
RA	Notthacker H.-P., Wang Z., Zhu Y., Reinscheid R.K., Lin S.H.S.,			
RA	Civelli O.;			
RT	"Molecular cloning and characterization of a second human cysteinyl			
RT	leukotriene receptor: discovery of a subtype selective agonist.";			
RL	Mol. Pharmacol. 58:1601-1608(2000).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22040266; PubMed=12044878; DOI=10.1016/S0014-5793(02)02775-8;			
RA	Takeda S., Kadowaki S., Haga T., Takasu H., Mitaku S.;			
RT	"Identification of G protein-coupled receptor genes from the human			
RT	genome sequence.";			
RL	FEBS Lett. 520:97-101(2002).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	Kopatz S.A., Aronstam R.S., Sharma S.V.;			
RT	"cDNA clones of human proteins involved in signal transduction			
RT	sequenced by the Guthrie cDNA resource center (www.cdna.org).";			

ALIGNMENTS

Q8bmj5 mus musculus
P43657 homo sapien
Q7z380 homo sapien
Q8bmc0 mus musculus
P41231 homo sapien
Q7z386 homo sapien
Q99677 homo sapien
Q6nsp5 homo sapien
Q8bkk1 mus musculus
O57466 melesgria g
Q57466 melesgria g
Q8bl22 rattus norv
Q8bl22 mus musculus
P21556 cavia porce

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RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RX PubMed=15057823; DOI=10.1038/nature02379;
RA Dunham A., Matthews L.H., Burton J., Ashurst J.L., Howe K.L.,
RA Ashcroft K.J., Beare D.M., Burford D.C., Hunt S.E.,
RA Griffiths-Jones S., Jones M.C., Keenan S.J., Oliver K., Scott C.E.,
RA Ainscough R., Almeida J.P., Ambrose K.D., Andrews D.T., Bannerjee R.,
RA Ashwell R.I.S., Babbage A.K., Bagguley C.L., Bailey J., Bannister R.,
RA Barlow K.F., Bates K., Beasley H., Bird C.P., Bray-Allen S.,
RA Brown A.J., Brown J.Y., Burrill W., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M.E., Clark S.Y., Clarke G., Clee C.M.,
RA Clegg S.C., Cobley V., Collins J.E., Corby N., Coville G.J.,
RA Deloukas P., Dhami P., Dunham I., Dunn M., Earthrowl M.E.,
RA Ellington A.G., Faulkner L., Frankish A.G., Frankland J., French L.,
RA Garner P., Garnett J., Gilbert J.G.R., Gilson C.J., Ghori J.,
RA Grafham D.V., Gribble S.M., Griffiths C., Hall R.E., Hammond S.,
RA Harley J.L., Hart E.A., Heath P.D., Howden P.J., Huckle E.J.,
RA Hunt P.J., Hunt A.R., Johnson C., Johnson D., Kay M., Kimberley A.M.,
RA King A., Laird G.K., Langford C.J., Lawlor S., Leongamornlert D.A.,
RA Lloyd D.M., Lloyd C., Loveland J.E., Lovell J., Martin S.,
RA Mashreghi-Mohammadi M., McLaren S.J., McMurray A., Milne S.,
RA Moore M.J.F., Nickerson T., Palmer S.A., Pearce A.V., Peck A.I.,
RA Pelan S., Phillimore B., Porter K.M., Rice C.M., Searle S.,
RA Sehra H.K., Showkeen R., Skuce C.D., Smith M., Steward C.A.,
RA Sycamore N., Tester J., Thomas D.W., Tracey A., Tromans A., Tubby B.,
RA Wall M., Wallis J.M., West A.P., Whitehead S.B., Willey D.B.,
RA Wilming L., Wray P.W., Wright M.W., Young L., Coulson A., Durbin R.,
RA Hubbard T., Sulston J.E., Beck S., Bentley D.R., Rogers J., Ross M.T.;
RT "The DNA sequence and analysis of human chromosome 13.";
RL Nature 428:522-528 (2004).
RN [7]
RP SEQUENCE OF 17-346 FROM N.A.
RA Suga H.;
RT "Homo sapiens cysteinyl leukotriene receptor 1 like receptor.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for cysteinyl leukotrienes. The response is
CC mediated via a G-protein that activates a phosphatidylinositol-
CC calcium second messenger system. Stimulation by BAY u9773, a
CC partial agonist, induces specific contractions of pulmonary veins
CC and might also have an indirect role in the relaxation of the
CC pulmonary vascular endothelium. The rank order of affinities for
CC the leukotrienes is LTC4 > LTD4 >> LTE4.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Widely expressed, with highest levels in the
CC heart, placenta, spleen, peripheral blood leukocytes and adrenal
CC gland. In lung, expressed in the interstitial macrophages, and
CC slightly in smooth muscle cells.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB038269; BAB03601.1; -
DR EMBL; AF254664; AAG17281.1; -
DR EMBL; AF279611; AAK69485.1; -
DR EMBL; AB083603; BAB89316.1; -
DR EMBL; AB083604; BAB89330.1; -
DR EMBL; AL137118; CAC29102.1; -
DR EMBL; AB041644; BAB16379.1; -
DR Genbank; HGNC:18274; CYSLTR2.
DR MIM; 605666; -
DR GO; GO:0004974; F-leukotriene receptor activity; NAS.
DR GO; GO:0006955; P-immune response; NAS.
DR InterPro; IPR004071; Cysleuk_receptor.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR01533; CYSLTR2RECPT.

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DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
FT DOMAIN 1 42 Extracellular (Potential).
FT TRANSMEM 43 63 1 (Potential).
FT DOMAIN 64 72 Cytoplasmic (Potential).
FT TRANSMEM 73 93 2 (Potential).
FT DOMAIN 94 123 Extracellular (Potential).
FT TRANSMEM 124 144 3 (Potential).
FT DOMAIN 145 153 Cytoplasmic (Potential).
FT TRANSMEM 154 174 4 (Potential).
FT DOMAIN 175 204 Extracellular (Potential).
FT TRANSMEM 205 225 5 (Potential).
FT DOMAIN 226 245 Cytoplasmic (Potential).
FT TRANSMEM 246 266 6 (Potential).
FT DOMAIN 267 286 Extracellular (Potential).
FT TRANSMEM 287 307 7 (Potential).
FT DOMAIN 308 346 Cytoplasmic (Potential).
FT DISULFID 111 187 By similarity.
FT CARBOHYD 20 20 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 26 26 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 30 30 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 181 181 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 346 AA; 39635 MW; EB54AA42DDCESEE4 CRC64;
Query Match 100.0%; Score 1712; DB 1; Length 346;
Best Local Similarity 100.0%; Pred. No. 5.9e-99;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEPNGTFSSNNRNCTIENFKREFPIVYLIITFFWGLVNGLSIYVFLQPKKSTSVNVP 60
DB 17 MEPNGTFSSNNRNCTIENFKREFPIVYLIITFFWGLVNGLSIYVFLQPKKSTSVNVP 76
QY 61 MLNLAIISDLFIISTLPFRADYYLRGNSMIFGDLACRIMSISLYSVNMYSSYIFLTVLVSVR 120
DB 77 MLNLAIISDLFIISTLPFRADYYLRGNSMIFGDLACRIMSISLYSVNMYSSYIFLTVLVSVR 136
QY 121 FLAMVHPRLHVTIRSASWILCGIWIILIMASSIMLDSGEQSGSVTSCLELNLYKIA 180
DB 137 FLAMVHPRLHVTIRSASWILCGIWIILIMASSIMLDSGEQSGSVTSCLELNLYKIA 196
QY 181 KLQTNWYIALVVGCLLPFTLSICYLLIIRVLKVEPESGLRVSHRKALTTIITLIIF 240
DB 197 KLQTNWYIALVVGCLLPFTLSICYLLIIRVLKVEPESGLRVSHRKALTTIITLIIF 256
QY 241 FLCFLPYHTLRTVHLTTWKVGLCKDLHLKALVITLALAAANACFNPLLYYFAGENFKDL 300
DB 257 FLCFLPYHTLRTVHLTTWKVGLCKDLHLKALVITLALAAANACFNPLLYYFAGENFKDL 316
QY 301 KSALRGHPQAKTKCVFPVSVWLKRETRV 330
DB 317 KSALRGHPQAKTKCVFPVSVWLKRETRV 346
RESULT 2
CLT2_FIG
ID CLT2_FIG STANDARD; PRT; 345 AA.
AC Q95N03;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cysteinyl leukotriene receptor 2 (CYSLTR2).
GN Name=CYSLTR2; Synonyms=CYSUT2;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]_TaxID=9823;
RP SEQUENCE FROM N.A.
RA Kamohara M., Takasaki J., Matsumoto M., Matsumoto S., Saito T.,
RA Ohishi T., Soga T., Matsushima H., Furuchi K.;
RT "Characterization of the cloned rat and porcine cysteinyl leukotriene

```

Db 317 LKSAALRGRPQ--KTRCGFSVCVWLKKETRV 345

RESULT 3

Q8R528	Q8R528	PRELIMINARY;	PRT;	309 AA.
ID	Q8R528	PRELIMINARY;	PRT;	309 AA.
AC	Q8R528;			
DT	01-JUN-2002 (T-EMBLrel. 21, Created)			
DT	01-JUN-2002 (T-EMBLrel. 21, Last sequence update)			
DT	01-MAR-2004 (T-EMBLrel. 26, Last annotation update)			
DE	Cysteinyln leukotriene 2 receptor.			
DE	Names=Cysltr2;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22013942; PubMed=11854273; DOI=10.1074/jbc.M109447200;			
RA	Ogasawara H., Ishii S., Yokomizo T., Kakinuma T., Komine M.,			
RA	Tamaki K., Shimizu T., Izumi T.;			
RT	"Characterization of Mouse Cysteinyl Leukotriene Receptors mCysLT1 and			
RT	mCysLT2. DIFFERENTIAL PHARMACOLOGICAL PROPERTIES AND TISSUE			
RT	DISTRIBUTION ";			
RL	J. Biol. Chem. 277:18763-18768(2002).			
DR	EMBL; AB058930; BAB86881.1; -.			
DR	MGD; MGI:1917336; Cysltr2.			
DR	GO; GO:0016021; C:integral to membrane; TAS.			
DR	GO; GO:0001631; F:cysteinyl leukotriene receptor activity; IDA.			
DR	InterPro; IPR004071; Cysleuk receptor.			
DR	InterPro; IPR000276; GPCR_Rhodpsn.			
DR	Pfam; PF00001; 7tm_1; 1.			
DR	PRINTS; PR01533; CYSLTRECPT.			
DR	PRINTS; PR00237; GPCR_RHODPSN.			
DR	PROSITE; PS0262; G_PROTEIN_RECPT_F1_2; 1.			
KW	Receptor.			
SQ	SEQUENCE 309 AA; 35226 MW; 96FACCB8AF6974 CRC64;			

Query Match 70.3%; Score 1204; DB 2; Length 309;

Best Local Similarity 73.4%; Pred. NO. 2e-67;

Matches 226; Conservative 30; Mismatches 52; Indels 0; Gaps 0;

QY	1	MEPNCGTFSNNRNCTIENFKREFFPIVLIIFFWGLGNGLSIYFLQPKKSTSVNVP	60
Db	1	MEVTGTPSSYSNNRNCTIENFKREFFPIIYLIIFFWGALGNFGSIYFLQTCCKSTSVNVP	60
QY	61	MLNLATSDLLFISTLPFRADYLRGSNWIFGDLACRIMSYSLVVMYSYIFLTVLSVVR	120
Db	61	MLNLATSDFLFISTLPFRADYYPFGSNWIFGDLACRWMSYSLVVMYSYIFLTVLSVVR	120
QY	121	FLAMVHPFRLLHVTYSIRSAWILCGIITWIMASSIMLLDSGSRQSGSVTSCLEINLYKIA	180
Db	121	FLATVHPFRMFHTSVRSAWILCGIIVWFIMASSALLVNGQEKDNIISCLELSPOKPK	180
QY	181	KLQTMNYIALVQCLLPFFTLTSCYLLIIRVLVKVEPSSGLRVSHRKALTITIIILIF	240
Db	181	SLLIIMNHIAVAGFLLPFLTLTTCYLLIIRLLKASIPESGPPAAHRKALTITIVAMITF	240
QY	241	FLCFLPHVTLRTVHLTTWKVGLCKDLRHKALVITLALAAANACFNPLLYYFAGENFKRL	300
Db	241	LLCFLPHALRTLUHLVTWDKSDGCVDLHKATVITLTMAAANSCFNPFLLYFAGENFKARL	300
QY	301	KSALRKGH 308	
Db	301	RAIFSKVH 308	

RESULT 4

CLT2_MOUSE	CLT2_MOUSE	STANDARD;	PRT;	309 AA.
AC	Q20A1;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			


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FT TRANSMEM 138 158 4 (Potential).
FT DOMAIN 159 187 Extracellular (Potential).
FT TRANSMEM 188 208 5 (Potential).
FT DOMAIN 209 229 Cytoplasmic (Potential).
FT TRANSMEM 230 250 6 (Potential).
FT DOMAIN 251 271 Extracellular (Potential).
FT TRANSMEM 272 292 7 (Potential).
FT DOMAIN 293 309 Cytoplasmic (Potential).
FT DISULFID 95 171 By similarity.
FT CARBOHYD 14 14 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 166 166 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 167 167 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 309 AA; 35507 MW; A122AC8177879D56 CRC64;

Query Match 69.3%; Score 1187; DB 1; Length 309;
Best Local Similarity 73.1%; Pred. No. 2.3e-66;
Matches 225; Conservative 26; Mismatches 57; Indels 0; Gaps 0;

QY 1 MEPNGTSSNNRNCTIENFKREFPIVYLIIFWGLVGNGLSIYVFLQPKKSTSVNVF 60
DB 1 MGVGTGTSYSDKNCTIENFKREFPIYIYLIIFWGLVGNGLSIYVFLQPKKSTSVNVF 60

QY 61 MLNLAIISDLFIETLPRADYVLRGSGNIWFGDLACRIMSYSLYNNMYSYIFLTVLSVR 120
DB 61 MLNLAIISDLFIETLPRADYVLRGSGNIWFGDLACRIMSYSLYNNMYSYIFLTVLSVR 120

QY 121 FLAMVHPFRLHVTIRSAILGCIWIILIMASSIMLLDSGSEONGSVTSCLEINLYKIA 180
DB 121 FLAMVHPFRLHVTIRSAILGCIWIILIMASSIMLLDSGSEONGSVTSCLEINLYKIA 180

QY 121 FLATNHPFQMLHITSVSAMILGCIWVFMASGLLLKKGKNTTICFELNLQKFK 180
DB 121 FLATNHPFQMLHITSVSAMILGCIWVFMASGLLLKKGKNTTICFELNLQKFK 180

QY 181 KLQTMNYIALVVGCLLPFTLSICYLIIIRVLLKVEPESGLRVSHRKALTTIITLIIF 240
DB 181 NLVLINLYALGVGLLPFTLSICYLIIIRVLLKVEPESGLRVSHRKALTTIITLIIF 240

QY 241 FLCPLPHTLRTVHLTWKVGKLCORLHKALVITLALAAANACNPLLYYPAGENFKRL 300
DB 241 LLCPLPHTLRTVHLTWKVGKLCORLHKALVITLALAAANACNPLLYYPAGENFKRL 300

QY 301 KSALRKQH 308
DB 301 RAIFSKDH 308

RESULT 6
CLTI RAT ID CLTI RAT STANDARD; PRT; 339 AA.
AC Q2476; 2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cysteinyln leukotriene receptor 1 (CysLTR1).
GN Name=CysLTR1; Synonyms=CysLTR;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Takasaki J., Kamohara M., Saito T., Matsumoto M., Matsumoto S.,
RA Ohishi T., Soga T., Matsushime H., Furuichi K.;
RT "Characterization of cloned rat and porcine cysteinyl leukotriene
RT receptors."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: Receptor for cysteinyl leukotrienes mediating
CC constriction of the microvascular smooth muscle during an
CC inflammatory response. This response is mediated via a G-protein
CC that activates a phosphatidylinositol-calcium second messenger
CC system [By similarity].
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
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CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; AB052685; BAB60825.1; -.
DR GGD; 619796; CysLTR1.
DR InterPro; IPR004071; Cysleuk receptor.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01533; CysLTR1.
DR PRINTS; PR0237; GPCR_Rhodopsin.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; FALSE_NEG.
DR PROSITE; PS00262; G PROTEIN RECEPTOR FL 2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
FT DOMAIN 1 30 Extracellular (Potential).
FT TRANSMEM 31 51 1 (Potential).
FT DOMAIN 52 59 Cytoplasmic (Potential).
FT TRANSMEM 60 80 2 (Potential).
FT DOMAIN 81 108 Extracellular (Potential).
FT TRANSMEM 109 129 3 (Potential).
FT DOMAIN 130 143 Cytoplasmic (Potential).
FT TRANSMEM 144 164 4 (Potential).
FT DOMAIN 165 195 Extracellular (Potential).
FT TRANSMEM 196 216 5 (Potential).
FT DOMAIN 217 232 Cytoplasmic (Potential).
FT TRANSMEM 233 253 6 (Potential).
FT TRANSMEM 254 278 Extracellular (Potential).
FT TRANSMEM 279 299 7 (Potential).
FT DOMAIN 300 339 Cytoplasmic (Potential).
FT DISULFID 98 175 By similarity.
FT CARBOHYD 171 171 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 339 AA; 39143 MW; 281841DF050DF8EA CRC64;

Query Match 33.1%; Score 567.5; DB 1; Length 339;
Best Local Similarity 36.7%; Pred. No. 7.8e-28;
Matches 122; Conservative 70; Mismatches 115; Indels 25; Gaps 8;

QY 6 TFSNNRNCTIENFKREFPIVYLIIFWGLVGNGLSIYVFLQPKKSTSVNVFMINLA 65
DB 10 TFSNNRNCTIENFKREFPIVYLIIFWGLVGNGLSIYVFLQPKKSTSVNVFMINLA 65

QY 66 ISDLFIETLPRADYVLRGSGNIWFGDLACRIMSYSLYNNMYSYIFLTVLSVVRFLAMV 125
DB 69 IADLLCVTLPLRVVYVHKWFGDFLCLRTYALYVLYNLCISIFPMTAMSPRCVAIV 128

QY 126 HPPRLHVTIRSAILGCIWI-LIMASSIMLLDSGSEONGSVTSCLEINLYKIAK--L 182
DB 129 FPVONINLVTKKARFVCGIWFILTSPPFLSKSYQDEKNTKCFEPPODKQTKYV 188

QY 183 QTMNYIALVVGCLLPFTLSICYLIIIRVLLKVEPESGLRVSHRKALTTIITLIIFL 242
DB 189 LVLYVSLYIFGFIPIFPIVTCYMTIITLLKNTMKKN--LPSSRRKAIIGMIIVTAAFLV 246

QY 243 CFLPYHTLRTVHL--TWKVGKLCORLHKALVITLALAAANACNPLLYYPAGENFKD 298
DB 247 SFNPHYIQRALHFLHSETRSCDSVLRMQKSVVITLSLAASNCDFPLLYFFSGGNFR 306

QY 299 RLKSLARK-----GHPQKATKTC 316
DB 307 RL-STFKHSLSSMTVIPKKKASLPKGBEMC 337

RESULT 7
CLTI RAT ID CLTI RAT STANDARD; PRT; 340 AA.
AC Q95N02;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cysteinyln leukotriene receptor 1 (CysLTR1).
DE
```


RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S., Krzyzanski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Receptor for cysteinyl leukotrienes mediating an
CC constriction of the microvascular smooth muscle during an
CC inflammatory response. This response is mediated via a G-protein
CC that activates a phosphatidylinositol-calcium second messenger
CC system. The rank order of affinities for the leukotrienes is LTD4
CC >> LTE4 = LTC4 >> LTC4.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Long;
CC IsoId=Q99JA4-1; Sequence=Displayed;
CC Name=2; Synonyms=Short;
CC IsoId=Q99JA4-2; Sequence=VSP_001921;
CC -1- TISSUE SPECIFICITY: Widely expressed, with higher expression in
CC the lung and skin, intermediate levels in the heart, kidney and
CC stomach and lower levels in several other tissues. Isoform 1 is
CC the most abundant form in all tested tissues.
CC -1- MISCELLANEOUS: MK-571, a selective antagonist, was shown to
CC inhibit eosinophilia, bronchial hyperreactivity and microvascular
CC leakage. Zafirlukast (Accolate) and pranlukast (Onon) were also
CC shown to be selective antagonists.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF329272; AAK16715.1; -
DR EMBL; AF329272; AAK16716.1; -
DR EMBL; AF205830; AAK15433.1; -
DR EMBL; AF263370; AAF73047.1; -
DR EMBL; AB044087; BAA96809.1; -
DR EMBL; BC027102; AAK27102.1; -
DR HSSP; P34996; IDDD.
DR MGD; MGI:1926218; Cysltr1.
DR GO; GO:0005887; C:integral to plasma membrane; IDA.
DR GO; GO:0004974; P:leukotriene receptor activity; IDA.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . . ; IDA.
DR InterPro; IPR004071; Cysleuk_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01533; CYSLTRCPTP.
DR PRINTS; PR00237; GPCR_RHODPSN.
DR PROSITE; PS00237; G PROTEIN RECP F1_1; FALSE_NEG.
DR PROSITE; PS00263; G_PROTEIN_RECP_F1_2; 1.
KW Alternative splicing; G-protein coupled receptor; Glycoprotein;
KW Transmembrane.
KW DOMAIN 1 43 Extracellular (Potential).
FT TRANSSEM 44 64 1 (Potential).
FT DOMAIN 65 72 Cytoplasmic (Potential).
FT TRANSSEM 73 93 2 (Potential).
FT DOMAIN 94 121 Extracellular (Potential).
FT TRANSSEM 122 142 3 (Potential).
FT DOMAIN 143 156 Cytoplasmic (Potential).
FT TRANSSEM 157 177 4 (Potential).
FT DOMAIN 178 208 Extracellular (Potential).
FT TRANSSEM 209 229 5 (Potential).
FT DOMAIN 230 245 Cytoplasmic (Potential).
FT TRANSSEM 246 266 6 (Potential).

FT DOMAIN 267 291 Extracellular (Potential).
FT TRANSSEM 292 312 7 (Potential).
FT DOMAIN 313 352 Cytoplasmic (Potential).
FT DISULFID 111 188 By similarity.
FT CARBOHYD 15 15 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 19 19 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 26 26 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 184 184 N-linked (GlcNAc. . .) (Potential).
FT VARSPLIC 1 13 Missing (in isoform 2).
FT CONFLICT 176 176 /FTId=VSP_001921.
FT CONFLICT 352 AA; 40715 MW; 5BDC94B3F1CD0CAB CRC64;
SQ SEQUENCE 32.7%; Score 560; DB 1; Length 352;
Query Match 38.5%; Pred. No. 2.3e-27;
Best Local Similarity 69; Mismatches 108; Indels 10; Gaps 6;
Matches 117; Conservative

QY 10 NNSRNCITENKREPPPIVLYLIFFWGLNGLSIYVFLQPKYKSTSVNFMNLAIADL 69
DB 26 NNTCHDTIDEFRNQVSTMYSVISVVGFGNPFVLYIKTYHEKSAFQVYMINLAIDL 85
QY 70 LFISTLPFRADYYLRGNSWIFGLACRIMSISLYVNNYSIYFILTIVLSVVRFLAMVHPPR 129
DB 86 LCVTPLRVRVYVHKWGLFGDFLCRLTYALYVNLVYCSIFPWTAMSPFCVAIVFPVQ 145
QY 130 LLHVTIRSAMILCGIWI-LIMASSIMLLDSGSENGSVTSCLNLYKIAX--LQTMN 186
DB 146 NINLVTKKARFVCIGIWIPIVILTSPFLMYKSVQDEKNTKCFEPQNNQAKYVILH 205
QY 187 YIALVVGCLLPFTLSICYLIIIRVLKVEPESGLRVSHRKALTTIILIFFLCLFLP 246
DB 206 YVSLPFGFIPIPTIIVCYVTMIITLLKNTMKCN--MPSRRKAIGMIIVVTAAPLVSFMP 263
QY 247 YHFLRTVHLFTW--KVGCLKD--RLHKALVITLALAAANACFNPPLYFAGENPKDLKS 302
DB 264 YHQRTHLLHLLHSETRPCDSVLRMQKSVVITLSLAASCCFDPPLLYFFSGGFRRL-S 322
QY 303 ALRK 306
DB 323 TFRK 326

RESULT 9
CLTI HUMAN STANDARD; PRT; 337 AA.
ID CLTI HUMAN
AC Q9Y271;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cysteinyl leukotriene receptor 1 (CysLTR1) (Cysteinyll leukotriene D4
DE receptor) (LTD4 receptor) (HG55) (HMTMF81).
GN Name=CysLTR1; Synonyms=CysLTR1;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tonsil;
RX MEDLINE=99318129; PubMed=10391245; DOI=10.1038/21658;
RA Lynch K.R., O'Neill G.P., Liu Q., Im D.-S., Sawyer N., Metters K.M.,
RA Coulombe N., Abramovitz M., Figueroa D.J., Zeng Z., Connolly B.M.,
RA Bai C., Austin C.P., Chateaufneuf A., Stocco R., Greig G.M.,
RA Kargman S., Hooks S.B., Hosfield E., Williams D.L. Jr.,
RA Ford-Hutchinson A.W., Caskey C.T., Evans J.F.;
RT "Characterization of the human cysteinyl leukotriene CysLTR1
RT receptor.";
RL Nature 399:789-793(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Leukocyte, Peripheral blood monocytes, and Spleen;
RX MEDLINE=99393629; PubMed=10462554;
RA Sarau H.M., Ames R.S., Chambers J., Ellis C., Elehourbagy N.,


```
FT DISULFID 106 183 By similarity.
FT CARBOHYD 10 10 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 23 23 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 176 176 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 179 179 N-linked (GlcNAc... ) (Potential).
FT CONFLICT 14 14 F -> L (in Ref. 5).
FT CONFLICT 236 236 K -> R (in Ref. 5).
SQ SEQUENCE 337 AA; 38251 MW; 6814EA0044756CE6 CRC64;

Query Match 28.5%; Score 487.5; DB 1; Length 337;
Best Local Similarity 34.9%; Pred. No. 7.3e-23;
Matches 111; Conservative 64; Mismatches 114; Indels 29; Gaps 10;

QY 14 NCTIEN--FKREFPPIVYLIIFFWGLNG--LSIVVF-LQPKKSTSVNFMNLAIAD 68
DQ 23 NCTDEIPLKQHVLPVIYGIIFVPGNAVISTYIFKMRPKSST---IIMNLACTD 79
QY 69 LLFISTLPFRADYYLGRNSWIFGDLACRIMSYSLYNNMYSSIVFLTVLSVVRFLAMVHPF 128
DQ 80 LLYLTSPLPIHYASGENWIFGDFMCKFIRFSHFENLYSSILFLTCFSLFRYVIVIHPM 139
QY 129 RLHVTSIRSAWILCGIHWILIMASSI---MLLDSGSEONGSVTSCLEL-NYKIAKLOT 184
DQ 140 SCFSIHKTRCAVAVACAVWVLIISLVAVIPMTFLTISTNRTNRSACLDLTSSDELNTIK--- 196
QY 182 LQTMVIALVVGCLLPFFLTSLICYLLIIRVLKVEPESGLRVSHRKALTIIITLIIF 241
DQ 197 --WYNILTATTTCPLPLVIVTCYTIITHTLTHGLQDSCLEK---QKARRLTILLLAFY 251
QY 242 LCFPLVHTLRTVHLTTWKVGL---CKDRLHKALVITLALAAANACFNPLLYYFAGNFKD 298
DQ 252 VCFPLPHILVRIRIESRLSISCSIEHQIEAVIVSRPLAALNTFGNLLYVVVSDNFQ 311
QY 299 RLKSAIR---KGHPQAK 313
DQ 312 AVCSTVRCKVSGNLEQAK 329

RESULT 12
Q6Y1R5
ID Q6Y1R5 PRELIMINARY; PRT; 337 AA.
AC Q6Y1R5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE G protein-coupled receptor 80.
GN Names=Gpr80;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX PubMed=15001573; DOI=10.1074/jbc.M400360200;
RA Imbe H., Watanabe S., Miyawaki M., Tanabe E., Encinas J.A.;
RT "Identification and Characterization of a Cell-Surface Receptor,
RT P2Y15, for AMP and Adenosine.";
RL J. Biol. Chem. 279:19790-19799(2004).
DR EMBL; AV191367; AAP32736.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045028; F:purinergic nucleotide receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR Rhodopsin.
DR InterPro; IPR002286; P2_puroceptor.
DR Pfam; PF00001; 7tm.1.1.
DR PRINTS; PRO0237; GFCRRHOOPS.
DR PRINTS; PRO1157; P2YPURNOCPTR.
DR PROSITE; PS0262; G_PROTEIN_RECPT_F1_2; 1.
KW Receptor.
SQ SEQUENCE 337 AA; 38377 MW; 98995E80DE0531CB9 CRC64;
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CC EMBL; U33447; AAB16746.1; -.
CC EMBL; Y12546; CAA73144.1; -.
CC EMBL; Z94154; CAB08107.1; -.
CC EMBL; Z94155; CAB08108.1; -.
CC HSP; P34996; IDDD.
CC Genew; HGNC:4471; GPR17.
CC H-invdb; HIX0002439; -.
CC MIM; 603071; -.
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0004950; F:chemokine receptor activity; TAS.
CC GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC InterPro; IPR002286; P2_purinoceptor.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODOPS.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Alternative splicing; G-protein coupled receptor; Glycoprotein; Transmembrane.
KW DOMAIN 1 64 Extracellular (Potential).
FT TRANSMEM 65 85 1 (Potential).
FT DOMAIN 86 92 Cytoplasmic (Potential).
FT TRANSMEM 93 113 2 (Potential).
FT DOMAIN 114 133 Extracellular (Potential).
FT TRANSMEM 134 154 3 (Potential).
FT DOMAIN 155 175 Cytoplasmic (Potential).
FT TRANSMEM 176 196 4 (Potential).
FT DOMAIN 197 223 Extracellular (Potential).
FT TRANSMEM 224 244 5 (Potential).
FT DOMAIN 245 260 Cytoplasmic (Potential).
FT TRANSMEM 261 281 6 (Potential).
FT DOMAIN 282 308 Extracellular (Potential).
FT TRANSMEM 309 329 7 (Potential).
FT DOMAIN 330 367 Cytoplasmic (Potential).
FT DISULFID 132 209 By similarity.
FT CARBOHYD 42 42 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 204 204 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 282 282 N-linked (GlcNAc. . .) (Potential).
FT VARSPLIC 1 28 Missing (in isoform 2).
FT /FTID=VSP_001987.
SQ SEQUENCE 367 AA; 40989 MW; 132FBE97BE83C60C CRC64;
Query Match 28.0%; Score 479; DB 1; Length 367;
Best Local Similarity 34.8%; Pred. No. 2.6e-22;
Matches 112; Conservative 62; Mismatches 126; Indels 22; Gaps 9;
QY 7 FSNNSRNCNTIEN-FKREPPPIVYLIIFFWGLVGLNGLSIYVLPQYKKSIVNVFMLNLA 65
DB 43 FSLATAEQCCQETPLENMFASFYLLDFILALVNTLALWFFIRDHKSGTPANVFLMHLA 102
QY 66 ISDLFLFTSLPFRADYYLRGSMWIFGDLACRINSYSLYVNMYSIYPLTIVLSVVRFLAMV 125
DB 103 VADLSCVLVLPTRLVYHFSGNHWPFGEIACRLGFLFLYLNWYASIVFLTICISADRFIAIV 162
QY 126 HPFRLLHVTIRSASWILCGIWIILI-MASSIMLLDSGSEQNGSVTSCLELNLYKIAKLOT 184
DB 163 HPVKSLLRRPLVLAHLACAFLLVWVAVAMAPLLVSPQTVQTNHTVVCLO--LYR-EKASH 219
QY 185 MNVIALVVGCLLPFTLSICVLIILVLLKVEPESGLRVSHR---KALTTIITLIIF 241
DB 220 HALVLSAVATFPFTTTCVLLIIRSL-----RQGLRVEKRLUKTKAVRMIAIVLAIFL 273
QY 242 LCFPYHTLRVLTHTLTKV--GLCKDRLHKALV--ITLAAANACPNLLYVFAGENFK 297
DB 274 VCFVPHVNRVSVVLYHRSHGASCATORILALANRITSLTSLNGALDPIMYFVAEKFR 333
QY 298 DRLKSAI-----RKGHPOKATK 315

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Db 334 HALCNLLGKRLKLPSPSPFEGK 355
RESULT 14
Q8N5S7 PRELIMINARY; PRT; 339 AA.
ID Q8N5S7
AC Q8N5S7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GPR17 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Spapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC031653; AAB31653.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045028; F:purinergic nucleotide receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR002276; GPCR_Rhodopsn.
DR InterPro; IPR002286; P2_purinoceptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PRINTS; PR01157; P2YPURNOCPTR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
SQ SEQUENCE 339 AA; 37860 MW; BB0CAFDF0FC371D63 CRC64;
Query Match 27.9%; Score 477; DB 2; Length 339;
Best Local Similarity 34.8%; Pred. No. 3.3e-22;
Matches 112; Conservative 61; Mismatches 127; Indels 22; Gaps 9;
QY 7 FSNNSRNCNTIEN-FKREPPPIVYLIIFFWGLVGLNGLSIYVLPQYKKSIVNVFMLNLA 65
DB 15 FSLATAEQCCQETPLENMFASFYLLDFILALVNTLALWFFIRDHKSGTPANVFLMHLA 74
QY 66 ISDLFLFTSLPFRADYYLRGSMWIFGDLACRINSYSLYVNMYSIYPLTIVLSVVRFLAMV 125
DB 75 VADLSCVLVLPTRLVYHFSGNHWPFGEIACRLGFLFLYLNWYASIVFLTICISADRFIAIV 134
QY 126 HPFRLLHVTIRSASWILCGIWIILI-MASSIMLLDSGSEQNGSVTSCLELNLYKIAKLOT 184
DB 135 HPVKSLLRRPLVLAHLACAFLLVWVAVAMAPLLVSPQTVQTNHTVVCLO--LYR-EKASH 191

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QY 185 MNVIALVVGCLLPFFTLISYLIILIRVLKVEVPESGLRVSHR---KALTIIITIIITLIIFP 241
Db 192 HALVSLAVAFPTFFITVTTCYLIIRSL-----ROGLRVEKRLKTKAVRMIAIVLAIFL 245
QY 242 LCFPLPHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACFNPLLYVFAGENFK 297
Db 246 VCFVPYVNRVVVLYHRSHGASCATQRIALANRITSCLTSLNGALDPMIMFFVFAEKPR 305
QY 298 DRLSAL-----RKGHPQKATK 315
Db 306 HALCNLLCGKRLKGPSPPEGK 327

RESULT 15
Q7ZZA4
ID Q7ZZA4 PRELIMINARY; PRT; 347 AA.
AC Q7ZZA4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE SI:bz46j2.9 (Novel protein similar to nucleotide receptors).
GN Name=pr2y41; Synonyms=SI:bz46j2.9, slc25a5;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Skuce C.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL590151; CAD68067.1; -.
DR ZFIN; ZDB-GENE-030616-77; pr2y41.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045028; F:purinergic nucleotide receptor activity; G-. . .; IEA.
DR GO; GO:004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR Rhodopsin.
DR InterPro; IPR000018; P2Y4 purinoceptor.
DR InterPro; IPR002286; P2_purinoceptor.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PRINTS; PR01066; P2Y4PRNOCPTR.
DR PRINTS; PR01157; P2YPRNOCPTR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 347 AA; 39861 MW; 3D3C01F83CC283E2 CRC64;

Query Match 27.9%; Score 477; DB 2; Length 347;
Best Local Similarity 32.3%; Pred. No. 3.3e-22;
Matches 102; Conservative 81; Mismatches 111; Indels 22; Gaps 10;

QY 14 NCTI-ENKREFFPIVYLIIFFWGLNGLSIYVF---LQPVKKSIVNVFVNLAIISDL 69
Db 11 SCTFDEEFYILLVSVSLVCFGLINSVALWMFITKRPWKRPST---VYMFHLALSDT 67
QY 70 LFISTLPFRADYYLRGNNIFGDLACRIMSYSLVNMYSIYFLTVLSVVRFLAMVHPFR 129
Db 68 LVVLSLPMLIYYVYANRSHNPFVGVLCIVRFLFYANLYCSILFLTCISVHYRVLGICHP 127
QY 130 LLHVTISRAWILCGIWIILIWASSI-MLLDGSEONGSVTSCLELNL-YKIAKIQTMNY 187
Db 128 SLTLIKPRAHMVCGFVMTAVIACLVPTLILVNTSRNGNSTLCHDTSRPEEFHNFVTYNS 187
QY 188 IALVGCCLLPFFTLISYLIILIRVLKVEVPESGL-----RVSHRKALTIIITLIIFP 242
Db 188 VMVLLFLPFLVIVVCYCLMARALCQ---PRKGLAQNOOSSRRKSIKLIIVLVVFAI 244
QY 243 CFLPHTLRTVHLTTWKV--GLCK--DRLHKALVITLALAAANACFNPLLYVFAGENFKD 298
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Db 245 CFVPPHITETLYY-AVRIFDADCKTLINIVNFSYKITRPLASVNSCLDPILYFLAGDHYRS 303
QY 299 RLKSALRKGHPOKAKT 314
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Job time : 961 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2005, 04:45:55 ; Search time 213 Seconds
(without alignments)
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Title: US-09-826-791A-1

Perfect score: 993

Sequence: 1 atggaacaaatggcactt.....gaaagaaacaagagtataa 993

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patent NA.*

- 1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
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- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	989.8	99.7	1401	US-09-585-876-1	Sequence 1, Appli
2	145.2	14.6	1578	US-09-044-404A-1	Sequence 1, Appli
3	145.2	14.6	1578	US-09-586-924-1	Sequence 1, Appli
4	99.4	10.0	1020	US-09-170-496D-31	Sequence 31, Appl
5	99.4	10.0	1900	US-09-016-434-1484	Sequence 1484, Ap
6	99.4	10.0	1901	US-08-153-848-43	Sequence 43, Appl
7	99.4	10.0	1901	US-09-299-843A-43	Sequence 43, Appl
8	99.4	10.0	1901	US-09-088-337B-43	Sequence 43, Appl
9	99.4	10.0	1901	5 PCT-US93-11153-43	Sequence 43, Appl
10	99.4	10.0	2453	US-09-085-07180-1	Sequence 181, App
11	96.2	9.7	1020	US-09-170-496D-181	Sequence 3, Appli
12	92	9.3	1255	US-08-097-938-3	Sequence 3, Appli
13	92	9.3	1255	US-08-476-000-3	Sequence 3, Appli
14	92	9.3	1255	US-08-472-840-3	Sequence 3, Appli
15	92	9.3	1255	US-08-476-976-3	Sequence 3, Appli
16	92	9.3	1255	US-08-474-410-3	Sequence 3, Appli
17	92	9.3	1255	US-08-486-673B-3	Sequence 3, Appli
18	90	9.1	1224	US-08-742-440A-1	Sequence 1, Appli
19	90	9.1	1414	US-08-476-000-62	Sequence 62, Appl
20	90	9.1	1414	US-08-472-840-62	Sequence 62, Appl
21	90	9.1	1414	US-08-476-976-62	Sequence 62, Appl
22	90	9.1	1414	US-08-474-410-62	Sequence 62, Appl
23	90	9.1	1414	US-08-486-673B-62	Sequence 62, Appl
24	85.6	8.6	1567	US-08-889-108-16	Sequence 16, Appl
25	85.6	8.6	1567	5 PCT-US94-10358-16	Sequence 16, Appl
26	85.6	8.6	2706	US-08-454-549-1	Sequence 1, Appli
27	85.6	8.6	2706	US-08-454-552-1	Sequence 1, Appli

28	85.2	8.6	1452	1	US-08-149-093A-3	Sequence 3, Appli
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30	85.2	8.6	1452	1	US-08-553-058C-3	Sequence 3, Appli
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32	85.2	8.6	1452	3	US-09-170-331-3	Sequence 3, Appli
33	85.2	8.6	1452	3	US-09-510-473-3	Sequence 3, Appli
34	85.2	8.6	1452	3	US-09-048-916B-3	Sequence 3, Appli
35	84.4	8.5	1551	4	US-09-016-434-1239	Sequence 1239, Ap
36	84.4	8.5	1551	4	US-09-023-655-1186	Sequence 1186, Ap
37	84.4	8.5	1780	4	US-09-054-272-1	Sequence 1, Appli
38	83.2	8.4	1098	4	US-09-170-496D-225	Sequence 225, App
39	82.4	8.3	2706	4	US-08-676-351-1	Sequence 1, Appli
40	81.6	8.2	1098	4	US-09-170-496D-117	Sequence 117, App
41	81.6	8.2	1597	2	US-08-724-974A-1	Sequence 26, Appl
42	81.6	8.2	1697	4	US-09-364-425B-26	Sequence 107, App
43	81.4	8.2	1164	4	US-09-170-496D-107	Sequence 221, App
44	81.4	8.2	1164	4	US-09-170-496D-221	Sequence 1259, Ap
45	81.4	8.2	2051	4	US-09-016-434-1259	

ALIGNMENTS

RESULT 1

US-09-585-876-1

; Sequence 1, Application US/09585876

; Patent No. 6586205

; GENERAL INFORMATION:

; APPLICANT: Glucksmann, Maria Alexandra

; APPLICANT: Silos-Santiago, Immaculada

; TITLE OF INVENTION: 43239, A No. 6586205el GPCR-Like Molecule and

; FILE REFERENCE: 5800-88

; CURRENT APPLICATION NUMBER: US/09/585,876

; CURRENT FILING DATE: 2000-06-01

; EARLIER APPLICATION NUMBER: 60/182,061

; EARLIER FILING DATE: 2000-02-11

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 1401

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (197)...(1237)

US-09-585-876-1

Query Match 99.7%; Score 989.8; DB 4; Length 1401;
Best Local Similarity 99.8%; Pred. No. 8.2e-307;
Matches 991; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	ATGCAACCAATGGCACCCTTCAGCAATAACACAGCAGGAACTGCACAAATTGAAACCTC 60
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Qy	61	AAGAGAGAATTTTCCCAATTTGATATCTGATAATATTTTCTGGGAGCTTTGGGAAAT 120
Db	305	AAGAGAGAATTTTCCCAATTTGATATCTGATAATATTTTCTGGGAGCTTTGGGAAAT 364
Qy	121	GGTTGTCCATATATGTTTTCCTGCAGCCTTATAAGAGTCCACATCTGTGAACGTTTC 180
Db	365	GGTTGTCCATATATGTTTTCCTGCAGCCTTATAAGAGTCCACATCTGTGAACGTTTC 424
Qy	181	ATGCTAAATCTGGCCATTTCCAGATCTCTGTTCCATAGCAGCTTCCCTTCAGGCTGAC 240
Db	425	ATGCTAAATCTGGCCATTTCCAGATCTCTGTTCCATAGCAGCTTCCCTTCAGGCTGAC 484
Qy	241	TATTATCTTAGAGGCTCCAATTTGGATATTTGGAGACCTGCGCTGCAGGATTATGCTTAT 300
Db	485	TATTATCTTAGAGGCTCCAATTTGGATATTTGGAGACCTGCGCTGCAGGATTATGCTTAT 544
Qy	301	TCCTTGTATGTCAAATGTACAGCAGTATTTATTTCTCTGACCGTGTGAGTGTGTGCGT 360

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Db 545 TCCTGTATGTAACATGTACAGCAGTATTAATTCCTGACCGTCTGAGTGTGTGGCT 604
Qy 361 TTCTTGGCATGTTTACCCCTTTGGCTTCTGCATGTACACAGCATCAGGAGTGCCTGG 420
Db 605 TTCTTGGCATGTTTACCCCTTTGGCTTCTGCATGTACACAGCATCAGGAGTGCCTGG 664
Qy 421 ATCTCTGTGGATCATATGATGATCCTTATCATGGCTTCTCAATAATGCTCCTGGACAGT 480
Db 665 ATCTCTGTGGATCATATGATGATCCTTATCAUGCTTCTCAATAATGCTCCTGGACAGT 724
Qy 481 GGCTCTGAGCAGAACGGCAGTGTACATCATGCTTAGAGCTGAATCTCTATATAAATTGCT 540
Db 725 GGCTCTGAGCAGAACGGCAGTGTACATCATGCTTAGAGCTGAATCTCTATATAAATTGCT 784
Qy 541 AAGCTCGACACCAATGAACATATATGCTTGGTGGTGGCTGCTGCGCATTTTTCACA 600
Db 785 AAGCTCGACACCAATGAACATATATGCTTGGTGGTGGCTGCTGCGCATTTTTCACA 844
Qy 601 CTGAGCATCTGTTATCTGCTGATCATTTCCGGTTCTGTTAAAGTGGAGGTCCCGAATCG 660
Db 845 CTGAGCATCTGTTATCTGCTGATCATTTCCGGTTCTGTTAAAGTGGAGGTCCCGAATCG 904
Qy 661 GGCTCGGGGTTTCTCACAGGAAGGCACTGACCAACCATCATCATCACCTTGATCATCTTC 720
Db 905 GGCTCGGGGTTTCTCACAGGAAGGCACTGACCAACCATCATCATCACCTTGATCATCTTC 964
Qy 721 TTCTTGTGTTCTGCTGCTTATCACACACTGAGGACCGTCCACTTGACGACATGGAAGTG 780
Db 965 TTCTTGTGTTCTGCTGCTTATCACACACTGAGGACCGTCCACTTGACGACATGGAAGTG 1024
Qy 781 GGTATTGCAAGACAGACTGCAATAAGCTTTGTTTATCACACTGGCGCTTGGCAGCAGCC 840
Db 1025 GGTATTGCAAGACAGACTGCAATAAGCTTTGTTTATCACACTGGCTTGGCAGCAGCC 1084
Qy 841 AATGCTGCTTCAATCCTCTGCTCTATTAATTTGCTGGGAGAAATTTTAAGGACAGACTA 900
Db 1085 AATGCTGCTTCAATCCTCTGCTCTATTAATTTGCTGGGAGAAATTTTAAGGACAGACTA 1144
Qy 901 AAGCTGCACTCAGAAAGGCCATCACAGNAGGCAAGCAAGTGTGTTTCCCTGTT 960
Db 1145 AAGCTGCACTCAGAAAGGCCATCACAGNAGGCAAGCAAGTGTGTTTCCCTGTT 1204
Qy 961 AGTGTGTGTTGAGAAAGGAAACAGAGTATAA 993
Db 1205 AGTGTGTGTTGAGAAAGGAAACAGAGTATAA 1237
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RESULT 2

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US-09-044-404A-1
; Sequence 1, Application US/09044404A
; Patent No. 6200775
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH
; APPLICANT: HALSEY, WENDY
; APPLICANT: ELLIS, CATHERINE
; APPLICANT: AMES, ROBERT
; APPLICANT: FOLEY, JAMES
; APPLICANT: SARAU, HENRY
; TITLE OF INVENTION: CDNA CLONE HMTMF81 THAT ENCODES
; TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 790 Swedeland Road, P.O. Box 1539
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
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; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/044,404A
; FILING DATE: MARCH 19, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/844,795
; FILING DATE: APRIL 22, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T.
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: GH-70001-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1578 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-044-404A-1
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Query Match 14.6%; Score 145.2; DB 3; Length 1578;
Best Local Similarity 51.5%; Pred. No. 1.1e-35;
Matches 451; Conservative 0; Mismatches 398; Indels 27; Gaps 4;

Qy 45 CACAATTGAAACTTCAAGAGAGAAATTTTCCCAATTTGTATATCTGATATAATTTTCTG 104
Db 514 CACTATTGATGACTTCCGCAATCAAGTGATTTCCACCTTGTACTCTATGATCTCTGTGT 573
Qy 105 GGGAGTCTTGGAAATGGTTGTCATATATGTTTCTGCGAGCCTTATAAGAAGTCCAC 164
Db 574 AGGCTTCTTTGGCAATGGCTTTGTGCTCTATGTCTCTATATAAAACCTATCAAGAAGTC 633
Qy 165 ATCTGTGAACGTTTTCATGCTAAATCTGGCCATTTCCAGATCTCCTGTTTCATAGCACGCT 224
Db 634 AGCCTTCCAGTATACATGATTAATTTAGCAGTAGCAGATCTACTTTGTGTGTGCACAT 693
Qy 225 TCCCTTCAAGGCTGACTATTTATCTTAGAGGCTCCAAATTTGGATATTTGGAGACCTGGCCTG 284
Db 694 GCCTCTCCGTGTGGTCTATTATGTCCACAAAGGCATTTGGCTCTTTGGTGACTTCTTGTG 753
Qy 285 CAGGATATGCTTATTCTTCTGTATGTCAACATGTACAGCAGTATTTATTTCTGACCGCT 344
Db 754 CGCCTCAGCACCTATGCTTTGTATGTCAACCTCTATTGTAGCATCTTCTTTATGACAGC 813
Qy 345 GCTGAGTGTGTGGCTTTTCTGGCAATGGTTCCACCCCTTTCCGGCTTCTGCATGTCAACCAG 404
Db 814 CATGAGCTTTTCCGGTGCATTTGCAATTTTCCAGTCCAGAACATTAATTTGGTTAC 873
Qy 405 CATCAGGAGTGCCTGGATCCTCTGTGGGATCATATGGATTCCTT--ATCATGGCTTCCTC 461
Db 874 ACAGAAAAAAGCCAGGTTGTGTGTAGGTATTTGGATTTTGTGATTTTGCACCATTC 933
Qy 462 AATAATGCTCTCGACAGCTGGCTCTGAGCAGAACGGCAGTGTACATCATGCTTAGAGCT 521
Db 934 TCCATTTCTAATGGCCAAACCAACAAAAGATGGGAAAAATAATACAAAGTCTTTGAGCC 993
Qy 522 GAATCTCTATAAAATTGCTAAGCTGCA-----GACCATGAACATATATTGCCCTTGGTGTG 575
Db 994 CCCACAAGACATCAAACTAAAAATCATGTTTTTGGTCTTGCATTTATGTGTCATTTGTTCT 1053
Qy 576 GGGCTGCTGCTGCCATTTTTCACACTCAGCATCTGTTATCTGTGATCATTTCCGGGTTCT 635
Db 1054 TGGCTTTTATCATCCCTTTTGTATTATAAATTTGCTGTGTACACAATGATCATTTTACCTT 1113
Qy 636 GTTAAAGTGGAGGTCCCGAGATCGGGGCTGGGGTTTCTCACAGGAAGGCACTGACAC 695
Db 1114 ACTAAAAAATCAATGAAAAAATAATCTGTCAAG-----TCATAAAAGGCTATAGGAAT 1167
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Db 218 TGGCCGTGGCCGACTTGTCTGCGTGTCTGCTCTGCCACCCGCCCTGGTCTACCACTTCT 277
Qy 251 GAGGCTCCATTTGGATATTTGGAGACTGGCCTGGAGGATATGCTTATTCCTTGTATG 310
Db 278 CTGGGAACCACTGGCCATTTGGGGAATCGCATGCGCTCTCACCGGCTTCTCTTCTACC 337
Qy 311 TCAACATGTACACAGTATTATTTCTGACCGTGTGAGTGTGTGCGTTTCTCTGGCAA 370
Db 338 TCAACATGTACACAGTATTATTTCTGACCGTGTGAGTGTGTGCGTTTCTCTGGCAA 397
Qy 371 TGGTTCAACCCCTTTCGGCTTCTGCATGTTCACACAGCATCAGGAGTGCCTGGATCTCTGTG 430
Db 398 TTGTGACCGGTCAGTCCCTCAAGCTCGCAGGCCCTCTACGCACACCTGGCCTGTG 457
Qy 431 GGATCATATGGATCTTATCATGGCTTCTCAATATGCTCTGGACAGTGGCTGTGAGC 490
Db 458 CTTCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 517
Qy 491 AGAACGGCAGTGTACATCATGTCTTAGAGCTGAATCTCTATAAAATTGCTAAGCTGCAGA 550
Db 518 TGCAGACCAACACACAGGTGGTCTGCTGAGCTGTACCGGGAGAAGGCTCCACCATG 577
Qy 551 CCATGAATATATGCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 610
Db 578 CCTGG-----TGTCCCTGGCAGTGGCCTTCACTTCCCGTTTCATCAACAGGTCACT 631
Qy 611 GTTATCTGCTGATCTTCCGGTCTCTGTTAAAGTGGAGTCCAGAACTGGGGTGGGG 670
Db 632 GCTACTGCTGATCATCCGAGCCTCGGAGGCTGCGTGGTGGAGAGCGCTCAAG- 690
Qy 671 TTTCTCACAGGAGGCACTGACCACTCATCATCACTTGATCATCTTCTTCTTCTTGT 730
Db 691 -----ACCAAGGAGTGGCATGATCGCCATAGTGTGGCCATCTTCTGGTCTGCT 742
Qy 731 TCTGCGCTTATCACACTGAGACCGTCCACTTG 765
Db 743 TGTGCGCTTACCAGTCAACCGCTCGTCTACGTG 777

RESULT 5

US-09-016-434-1484
; Sequence 1484, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1484:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1900 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g992699
; US-09-016-434-1484

Query Match 10.0%; Score 99.4; DB 4; Length 1900;

Best Local Similarity 48.8%; Pred. No. 6.1e-21;
Matches 339; Conservative 0; Mismatches 341; Indels 15; Gaps 2;

Qy 71 TTTTCCCAATTGTATATCTGATAATATTTTCTGGGGAGTCTTGGGAAATGGTGTGTCCA 130
Db 797 TGTTCGCCCTCTTCTACCTTCTGGATTTTATCTGGCTTTAGTTGGCAATACCTGGCTC 856
Qy 131 TATATGTTTTCTGAGCCTTATAAGAGTCCACATCTGTGAACGTTTTTTCATGCTAAATC 190
Db 857 TGTGGCTTTTTCATCCGAGACCAAGTCCGGGACCCCGGCCAACGTTTCTCTGATGCATC 916
Qy 191 TGGCCATTTTCAGATCTCCTGTTTCATAAGCACGCTTCCCTTCAGGGCTGACTATATCTTA 250
Db 917 TGGCCGTGGCCACTTTGTCGCGTGTGGTCTTGCCTCCACCCGCTTGTCTTACCTTCT 976
Qy 251 GAGGCTCCAAATTGGATATTTGGAGACCTGGCCTGCAGGATATATGCTTATTCCTTGTATG 310
Db 977 CTGGGAAACACTGGCCATTTGGGGAATCGCATGCCGTCTCACCGCTTCTCTTCTACC 1036
Qy 311 TCAACATGTACAGCAGTATTATTTCTGACCGTGTGAGTGTGTGCGTTTCTCTGGCAA 370
Db 1037 TCAACATGTACGCCAGCATCTACTTCTCACCTGTGATCAGCGCCGACCGCTTCTCTGGCCA 1096
Qy 371 TGGTTCAACCCCTTTCGGCTTCTGCATGTCCACAGCATCAGGAGTGCCTGGATCCTCTGTG 430
Db 1097 TTGTGACCCCGTCAAGTCCCTCAAGCTCCGAGGCCCTCTACGCACACCTGGCTGTG 1156
Qy 431 GGATCATATGGATCCTTATCATGGCTTCTCAATAATGCTCCTGGACAGTGGCTCTGAGC 490
Db 1157 CTTCTCTGTGGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1216
Qy 491 AGAAGCGCAGTGTACATCATCTTAGAGCTGAATCTCTATAAAATTGCTAAGTGTGCGAG 550
Db 1217 TGCAGACCAACCAACACCGGTGTCTGCTGACGTGTACCGGGAGAAGGCTTCCACCATG 1276
Qy 551 CCATGAACATATATTCGCTTGGTGGGCTGCTGTGCAATTTTTCACACTCAGCATCT 610
Db 1277 CCTGG-----TGTCCCTGGCAGTGGCCTTCACTTCCCGTTTCATCACCAGGTCACT 1330
Qy 611 GTTATCTGCTGATCATTCGGTCTTGTATAAAGTGGAGTCCAGAAATCGGGGCTGCGGG 670
Db 1331 GCTACTGCTGATCATCCGACGCTCGGCGAGGCTGCGTGTGGAGAAGCGCTCAAG- 1389
Qy 671 TTTCTCACAGGAAGCAGTACACCAATCATCATCTTGTATCATCTTCTTCTTGTGT 730
Db 1390 -----ACCAAGGAGTGGCAGTGCATGCGCCATAGTGTGCGCCATCTTCTTGGTCTGCT 1441
Qy 731 TCTGCGCTTATCACACACTGAGGACCGTCCACTTG 765
Db 1442 TGTGCGCTTACCACGTCACCGCTCGTCTACGTG 1476

RESULT 6

US-08-153-848-43
; Sequence 43, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald


```

Db      1158  CCTTCTGTGGGTGGTGGCTGTGGCCATGCGCCCGCTGCTGGTGAGCCACAGACCG 12117
Qy      491  AGAACGGCAGTGTACATCATGCTTAGAGCTGAATCTCTATAAAATTGCTAAAGTGCAGA 550
Db      1218  TGCAGACCAACACACACGGTGGTCTGCCTCTGAGCTGTACCGGAGAAAGCGCTCCACCATG 12777
Qy      551  CNAATGAACATATATTGCTTGGTGGTGGCTGCTGCTGCCATTTTTCACACTCAGCATCT 610
Db      1278  CCCTGG-----TGTCCCTGGCAGTGGCCCTTACCTTCCTCCGTTTCATCACACCGTCACCT 1331
Qy      611  GTTATCTGCTGATCATTTCCGGTTCTGTATAAAGTGGAGGTGCCAGAAATCGGGGCTGCGGG 670
Db      1332  GCTACTCTGCTGATCATCCGAGCCTCGGCAGCGGCTGCGTGTGGAGAGCGGCTCAAG- 1390
Qy      671  TTTCTCACAGGAGGCATGACACCATCATCATCATCACTTGTATCATCTTCTTCTTGTGTT 730
Db      1391  -----ACCAAGGCAGTGGCGATCATCGCCATAGTGTGGCCATCTTCTCTGTCTGCT 1442
Qy      731  TCCTGCCCTATCACACACTGAGGACCGTCCACTTG 765
Db      1443  TCGTGGCCCTACCAAGCTCAACCGCTCCGCTACGTG 1477

RESULT 7
US-09-299-843A-43
; Sequence 43, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1901 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

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/ FILING DATE: 06-JUNE-1995
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: MULLINS, J.G.
/ REGISTRATION NUMBER: 30,073
/ REFERENCE/DOCKET NUMBER: 325800-366
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 201-994-1700
/ TELEFAX: 201-994-1744
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2453 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 548..1564
PCT-US95-07180-1

Query Match 10.0%; Score 99.4; DB 5; Length 2453;
Best Local Similarity 48.8%; Pred. No. 7.2e-21;
Matches 339; Conservative 0; Mismatches 341; Indels 15; Gaps 2;
71 TTTTCCCAATTGTATCTGATAATAATTTTCTGGGAGTCTTTGGGAAATGGGTTCTGCCA 130
Db |||||
645 TGTTCGGCTCCTTCTACCTCTCGATTTTATCTGCGCTTAGTTGGCAATACCTCGGCTC 704
Qy 131 TATATGTTTCTGCGAGCCTTATPAGAAGTCCACATCTGTGAACGTTTTCATGCTAAATC 190
Db |||||
705 TGTGGCTTTTCATCCGAGACCAAGTCCGGGACCCCGGCCAACGTTGTTCTGATGCATC 764
Qy 191 TGGCCATTTTCAGATCTCCTGTTTATGAACAGCTTCCCTTCAGGCTGACTATTATCTTA 250
Db |||||
765 TGGCCGTGGCGCACTTGTGTGGTGTGCTGCTGCCACCCCGCCCTGGCTACCACTTCT 824
Qy 251 GAGGCTCCAAATGGATATTTGGAGACTGGCCCTGCAGAGTATATGTTTATCTTCTGATG 310
Db |||||
825 CTGGGAACCACTGGCCATTTGGGGAATCGCATGCCGTCTCACCGGCTTCTCTTACC 884
Qy 311 TCAACATGTACAGCAGTATTTATTTCTGACCGTGTGAGTGTGTGCGTTTCTGGCAA 370
Db |||||
885 TCAACATGTACGCGCAGCATCTACTTCTCACCTGTCATCAGCGCGCACCGTTTCTGGCCA 944
Qy 371 TGGTTACCCCTTTCGGCTTCTGCATGTCCACAGCATCAGGAGTGCCTGGATCCTCTGTG 430
Db |||||
945 TTGTGACCCGGTCAAGTCCCTCAAGCTCCGACGGCCCTCTACGCACACACCTGGGCTGTG 1004
Qy 431 GGATCATATGGATCCTTATCATGGCTTCTCAATAATGCTCTGGACAGTGGCTCTGAGC 490
Db |||||
1005 CCTTCTGTGGTGGTGGTGGTGTGGCCATGGCCCGCTGCTGGTGAGCCACAGACCG 1064
Qy 491 AGAAGCGCAGTGTCAATCATGCTTAGAGCTGAATCTCTATAAAATTTGTAAGCTGCAGA 550
Db |||||
1065 TGCAGACCAACCAACCGGTGTGCTGCTGCAGTGTACCGGAGAGGCTTCCACCATG 1124
Qy 551 CCATGAATATATGCTTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 610
Db |||||
1125 CCCTGG-----TGTCCCTGGAGTGGCTTACCTTCCCGTTTCATCAGCAGGTCACCT 1178
Qy 611 GTTATCTGTGATCATTCGGGTTCTGTATAAAGTGGAGGTCCAGAAATCGGGGCTCGGG 670
Db |||||
1179 GCTACCTGTGATCATCCGAGCCTCGGCGAGGCTGCTGTGGAGAGCGGCTCAAG- 1237
Qy 671 TTTCTCAGAGGAGGAGCTGACACCATCATCATCATCATCATCATCATCATCATCATCATCAT 730
Db |||||
1238 -----ACCAAGGAGTGGCATATGCCATAGTGTGGCCATCTTCTGGTCTGCT 1289
Qy 731 TCCTGCCCTATCACACTGAGGACGTCACCTTG 765
Db |||||
1290 TCGTGGCTTACCACGTCACCGCTCCGTTCTACGTG 1324

RESULT 11
US-09-170-496D-181
/ Sequence 181, Application US/09170496D
/ Patent No. 6555339
/ GENERAL INFORMATION:
/ APPLICANT: Behan, Dominic P.
/ APPLICANT: Chalmers, Derek T.
/ APPLICANT: Liaw, Chen W.
/ TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-C
/ TITLE OF INVENTION: Receptors
/ FILE REFERENCE: AREN-0040
/ CURRENT APPLICATION NUMBER: US/09/170,496D
/ CURRENT FILING DATE: 1998-10-13
/ NUMBER OF SEQ ID NOS: 294
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 181
/ LENGTH: 1020
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-170-496D-181

Query Match 9.7%; Score 96.2; DB 4; Length 1020;
Best Local Similarity 48.5%; Pred. No. 4.4e-20;
Matches 337; Conservative 0; Mismatches 343; Indels 15; Gaps 2;
71 TTTTCCCAATTGTATCTGATAATAATTTTCTGGGAGTCTTTGGGAAATGGGTTCTGCCA 130
Db |||||
98 TGTTCGGCTCCTTCTACCTTCTGGATTTTATCTGCGCTTAGTTGGCAATACCTCGGCTC 157
Qy 131 TATATGTTTCTGCGAGCCTTATAAGAAGTCCACATCTGTGAACGTTTTCATGCTAAATC 190
Db |||||
158 TGTGGCTTTTCATCCGAGACCAAGTCCGGGACCCCGGCCAACGTTGTTCTGATGCATC 217
Qy 191 TGGCCATTTTCAGATCTCCTGTTTATGAACAGCTTCCCTTCAGGCTGACTATTATCTTA 250
Db |||||
218 TGGCCGTGGCGCACTTGTGCTGCTGCTGCCACCCCGCCCTGGCTACCACTTCT 277
Qy 251 GAGGCTCCAAATGGATATTTGGAGACTGGCCCTGCAGAGTATATGTTTATCTTCTGATG 310
Db |||||
278 CTGGGAACCACTGGCCATTTGGGGAATCGCATGCCGTCTCACCGGCTTCTCTTACC 337
Qy 311 TCAACATGTACAGCAGTATTTATTTCTGACCGTGTGAGTGTGTGCGTTTCTGGCAA 370
Db |||||
338 TCAACATGTACGCCAGCATCTACTTCTCACCTGTCATCAGCGCGCACCGTTTCTGGCCA 397
Qy 371 TGGTTACCCCTTTCGGCTTCTGCATGTCCACAGCATCAGGAGTGCCTGGATCCTCTGTG 430
Db |||||
398 TTGTGACCCGGTCAAGTCCCTCAAGCTCCGACGGCCCTCTACGCACACACCTGGGCTGTG 457
Qy 431 GGATCATATGGATCCTTATCATGGCTTCTCAATAATGCTCTGGACAGTGGCTCTGAGC 490
Db |||||
458 CCTTCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 517
Qy 491 AGAAGCGCAGTGTCAATCATGCTTAGAGCTGAATCTCTATAAAATTTGTAAGCTGCAGA 550
Db |||||
518 TGCAGACCAACCAACCGGTGTGCTGCTGCAGTGTACCGGAGAGGCTTCCACCATG 577
Qy 551 CCATGAATATATGCTTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 610
Db |||||
578 CCCTGG-----TGTCCCTGGAGTGGCTTACCTTCCCGTTTCATCAGCAGGTCACCT 631
Qy 611 GTTATCTGTGATCATTCGGGTTCTGTATAAAGTGGAGGTCCAGAAATCGGGGCTCGGG 670
Db |||||
632 GCTACCTGTGATCATCCGAGCCTCGGCGAGGCTGCTGTGGAGAGCGGCTCAAG- 690
Qy 671 TTTCTCAGAGGAGGAGCTGACACCATCATCATCATCATCATCATCATCATCATCATCATCAT 730
Db |||||
691 -----ACCAAGGAGTGGCATATGCCATAGTGTGGCCATCTTCTGGTCTGCT 742
Qy 731 TCCTGCCCTATCACACTGAGGACGTCACCTTG 765
Db |||||
743 TCGTGGCTTACCACGTCACCGCTCCGTTCTACGTG 777

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RESULT 12
US-08-097-938-3
; Sequence 3, Application US/08097938
; Patent No. 5629174
; GENERAL INFORMATION:
; APPLICANT: SUNDELIN, JOHAN
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR AND ITS
; TITLE OF INVENTION: AGONISTS AND ANTAGONISTS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,938
; FILING DATE: 26-JUL-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22803-20006.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1255 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 56..1249
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 56
US-08-097-938-3

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Query Match	9.3%;	Score 92;	DB 1;	Length 1255;
Best Local Similarity	54.4%;	Pred. No. 1.1e-18;		
Matches 185;	Conservative 0;	Mismatches 155;	Indels 0;	Gaps 0;
QY	49	ATTGAANA	CTCAAGAGAGAA	TTTTTCCCAATTCGTATATCTGATAAATATTTTCTGGGGA 108
DB	266	ACTGGAAA	CTGACCACCTG	CTTCCCTTCCCAATTCGTACAAATGTGTTGTGGTGGGT 325
QY	109	GTCTTGGG	AAATGGTGTGC	ATATATGTTTTCTCGCAGCCTTATAAGAACTCCACATCT 168
DB	326	TTGCCAAG	TACGGCATGG	CCCTCTTTCTTTCGAACTAAGAAGACACCCCT 385
QY	169	GTGAACG	TTTTTCATGCT	TAATCTGGCCATTTTCAGATCTCTGTTTCATAAGCACGCTTCCC 228
DB	386	GCTGTG	ATTACATGG	CCCAATCTGGCCTTGGCTGACCTCTCTCTGTCACTGTGTTCCCC 445
QY	229	TTCAGG	CGCTGAC	TATTAATCTTAGAGGCTCCAAATTTGGATAATTTGAGACCTTGGCCCTGCAGG 288
DB	446	TTGAAG	ATTGCC	TATCACATACATACATGGCAACAACTGGATTTATGGGAAGCTCTTTTGTAAAT 505
QY	289	ATTATG	CTCTATTC	CTTGTATGTCACATGTACAGCAGTATTTATTTCTTGACCGTGTCTG 348
DB	506	GTGCTT	ATTGGCT	TTTTCTATGGCAACATGTACTGTTCCATTTCTTTCATGACCTGCCTC 565

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349 AGTGTGTGCGTTCCTGGCAATCGATTTCACCCCTTTCCGGC 388
||||| ||||| ||||| ||||| ||||| ||||| |||||
566 AGTGTGCAGAGGTATTGGGTCAATCGTGAACCCCATGGGC 605
||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
US-08-476-000-3
; Sequence 3, Application US/08476000
; Patent No. 5716789
; GENERAL INFORMATION:
; APPLICANT: SUNDELIN, JOHAN
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS A
; TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACI
; TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACI
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,000
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/390,301
; FILING DATE: 25-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: ADLER, REID G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 2803-0006.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1255 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 56..1249
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 56
; US-08-476-000-3

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Query Match	9.3%	Score 92	DB 1	Length 1255
Best Local Similarity	54.4%	Pred. No. 1.1e-18		
Matches 185	Conservative 0	Mismatches 155	Indels 0	Gaps 0
Qy	49	ATTGAAACTTCAAGAGAGAATTTTCCCAATGTATATCTGATAATATTTCTGGGGA	108	
Db	266	ACTGGAACACTGACCTGCTCTCTTCCCAATGTCTACAAATGTGTTGTGGTGGT	325	
Qy	109	GTCTTGGGAAATGGGTGTGCCATATATGTTTTCTCGAGCCTTATAAGAAAGTCCACATCT	168	
Db	326	TTGCCAAGTAACGGCATGGCCCTGTGGGTCTTTCTTTCCGAACTAAGAAAGACACCT	385	
Qy	169	GTGAAAGTTTTATGCTTAATCTGGCCATTTAGATCTCTGTTCATTAAGCAGCGTTCCC	228	
Db	386	GCTGTGATTTACATGGCCAACTGTGGCCTCTGGCTGACCTCTCTGTGTCATCTGGTTC	445	
Qy	229	TTCAGGCGCTGACTATTATCTTTAGAGGCTCCAAATTGGATATTTGGAGACCTTGGCCTGCAGG	288	

Db 446 TTGAAGATGCCTATCACATACATGGCAACAATGGATTATGGGAAGCTCTTGTAAAT 505
QY 289 ATTATGCTTATTCCTTGATGCAACATGACAGCAGTATTTATTTCTGACCGTGTG 348
Db 506 GTGCTTATTGGCTTTTCTATGGCAACATGACTGTTCCATTCTCTTCATGACCTGCCTC 565
QY 349 AGTGTGTGCTTCTCTGCAATGGTTCAACCCCTTTCCGC 388
Db 566 AGTGTGACAGGTATTGGGTGTCATCGTGAACCCCATGGGGC 605

RESULT 14
US-08-472-840-3
; Sequence 3, Application US/08472840
; Patent No. 5763575
; GENERAL INFORMATION:
; APPLICANT: SUNDELIN, JOHAN
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
; TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,840
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,301
; FILING DATE: 25-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: ADLER, REID G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 2803-0006.20
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1255 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 56..1249
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 56
US-08-472-840-3

Query Match 9.3%; Score 92; DB 1; Length 1255;
Best Local Similarity 54.4%; Pred. No. 1.1e-18;
Matches 185; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

QY 49 ATTGAAACTTCAAGAGAGAATTTTCCCAATTGATATCTGATAATTTTCTGGGGA 108
Db 266 ACTGGAAACTGACCACTGCTCTCTCCATTTGCTACACATTTGTTGTGGTGGT 325
QY 109 GTCTTGGGAAATGGGTGTGCCATATATGTTTCTGACGCTTATAAGAGTCCACATCT 168

Db 326 TTGCCAAGTAACGGCATGSCCCTGTGGGTCTTTCTTTTCCGAACTAAGAAGACACCCT 385
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QY 349 AGTGTGTGCGTTCCTGCAATGGTTCAACCCCTTTCCGC 388
Db 566 AGTGTGACAGGTATTGGGTGTCATCGTGAACCCCATGGGGC 605

RESULT 15
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; Sequence 3, Application US/08476976
; Patent No. 5874400
; GENERAL INFORMATION:
; APPLICANT: SUNDELIN, JOHAN
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
; TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,976
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/390,301
; FILING DATE: 25-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: ADLER, REID G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 2803-0006.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1255 base pairs
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Matches 185; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

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Search completed: August 20, 2005, 07:35:01
Job time : 217 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2005, 04:38:00 ; Search time 3256 Seconds
(without alignments)

11608.667 Million cell updates/sec

Title: US-09-826-791A-1

Perfect score: 993

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Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:

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3: gb_hic.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	675	68.0	758	6	CD630086
3	666	67.1	762	6	CD630084
4	663	66.8	745	6	CD630072
5	661.2	66.6	726	6	CD630089
6	632	63.6	753	6	CD630075
7	619.2	62.4	750	6	CD630077
8	618	62.2	673	6	CD630069
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10	603	60.7	652	6	CD630079
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18	521	52.5	844	6	CD630082
C 19	515.6	51.9	860	6	CD630070
C 20	505	50.9	848	6	CD630090
C 21	478.8	48.2	827	6	CD630073
C 22	470.8	47.4	798	6	CD630076
C 23	463	46.6	808	6	CD630088
C 24	457.8	46.1	809	6	CD630068

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C 28	412	41.5	735	6	CD630085
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C 33	301.2	30.3	319	8	AQ001459
C 34	179.4	18.1	604	1	A1178926
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C 36	146.8	14.8	996	3	CL092116
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ALIGNMENTS

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IMAGE:7389737 3', mRNA sequence.
ACCESSION C0959137
VERSION C0959137.1 GI:51323719
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabs-x@mail.nih.gov
Tissue Procurement: Guthrie cDNA Resource Center
cDNA Library Preparation: Guthrie cDNA Resource Center
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: INB17 row: f column: 03
High quality sequence start: 20
High quality sequence stop: 632.

FEATURES

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/clone="IMAGE:7389737"
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/lab_host="DH10B (T1-phage-resistant)"
/clone_lib="NIH_MGC_146"
/notes="Vector: pCDNA3.1; Site 1: multiple; Site 2: multiple; ORF's were PCR-amplified (from IMAGE clones or from commercially available cDNA libraries) and cloned by the Guthrie cDNA Resource Center (www.guthrie.org/cDNA) into pCDNA3.1. For specific information on cloning sites (which vary by clone), please refer to the Guthrie website, using the Guthrie ID given in the file

ftp://image.llnl.gov.image.rearrayed_plates/IRBF_presv.dat
a. Note: this is a NIH_MGC Library."

ORIGIN		Query Match 69.8%; Score 693; DB 7; Length 720; Best Local Similarity 99.9%; Pred. No. 3e-190; Matches 704; Conservative 0; Mismatches 0; Indels 1; Gaps 1;	
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QY	528	CTATAAAATTGCTAAGCTGCAGACCATGAATATATTGGCTTGGTGGCTGCCTGCT	587
Db	480	CTATAAAATTGCTAAGCTGCAGACCATGAATATATTGGCTTGGTGGCTGCCTGCT	421
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QY	708	CTTGATCATCTTCTTGTGTTTCTCGCTTATCAACACTGAGGACCGTCCACTTTGAC	767
Db	300	CTTGATCATCTTCTTGTGTTTCTCGCTTATCAACACTGAGGACCGTCCACTTTGAC	241
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Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L. Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes Genomics 84 (1), 205-210 (2004)			
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Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L. Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes Genomics 84 (1), 205-210 (2004)			
REFERENCE			
AUTHORS			
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JOURNAL			
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Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L. Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes Genomics 84 (1), 205-210 (2004)			
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Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L. Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes Genomics 84 (1), 205-210 (2004)			
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Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L. Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes Genomics 84 (1), 205-210 (2004)			
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Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L. Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes Genomics 84 (1), 205-210 (2004)			
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JOURNAL			
CD630086			
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SOURCE			

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KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 762)
JOURNAL Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
COMMENT Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
FEATURES source
Location/Qualifiers
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/clone_lib="FLP"
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Best Local Similarity 99.4%; Pred. No. 2.3e-182;
Matches 700; Conservative 0; Mismatches 0; Indels 4; Gaps 3;
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DB 50 ATGGAACCAATGGCACCTTCAGCAATTAACAACAGCAGGAAGTGCACAAATTGAAACTTC 109
QY 61 AAGAGAGAATTTTCCCAATTTGATATCTGATATATATTTTCTGGGGAGTCTTGGGAAAT 120
DB 110 AAGAGAGAATTTTCCCAATTTGATATCTGATATATATTTTCTGGGGAGTCTTGGGAAAT 169
QY 121 GGTTGTGCCATATATGTTTCTCGAGCCTTATAAGAAAGTCCACATCTGTGAACGTTTTTC 180
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DB 230 ATGCTTAATCTGGCCATTTCCAGATCTCTGTTTCAATAGCAGCTTCCCTTCAGGGCTGAC 289
QY 241 TATTATCTTAGAGCTCCAAATTTGGATATTTTGGAGACCTGGCTTCAGGATTTATGCTTAT 300
DB 290 TATTATCTTAGAGCTCCAAATTTGGATATTTTGGAGACCTGGCTTCAGGATTTATGCTTAT 349
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QY 361 TTCTTGGCAATGGTTACCCCTTTCCGCTTCTGATGTCACGATCAGGAGTGCCTGG 420
DB 410 TTCTTGGCAATGGTTACCCCTTTCCGCTTCTGATGTCACGATCAGGAGTGCCTGG 469
QY 421 ATCTCTGTGGGATCATATGGATCTTATCATGGCTTCTCAATAATGCTCCTGGACAGT 480
DB 470 ATCTCTGTGGGATCATATGGATCTTATCATGGCTTCTCAATAATGCTCCTGGACAGT 529
QY 481 GGCTCTGAGCAGAACCGCAGTGTACATCATGCTTAGAGCTGAATCTCTATAAAATTTGCT 540
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QY 541 AAGCTGAGACCATGAATATATGGCTTGGTGGTGGCTGCC--TGCTGCCATTTTTCAC 599
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QY 600 ACTCAGCATCTGTTATCTGCTGATCATATCGGGTTCTGTTA--AAAGTGGAGGT--CCGAGA 656
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QY 657 ATCGGGGCTCGGGGTTTCTCACAGGAAGGCACTGACCATCA 700
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RESULT 4
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DEFINITION 5603992J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD630072
VERSION CD630072.1 GI:40278338
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 745)
JOURNAL Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
COMMENT Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
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Location/Qualifiers
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/organism="Homo sapiens"
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/clone_lib="FLP"
/notes="Vector: pDrive Cloning Vector"
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Best Local Similarity 99.7%; Pred. No. 1.7e-181;
Matches 685; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
QY 1 ATGGAACCAATGGCACCTTCAGCAATTAACAACAGCAGGAAGTGCACAAATTGAAACTTC 60
DB 50 ATGGAACCAATGGCACCTTCAGCAATTAACAACAGCAGGAAGTGCACAAATTGAAACTTC 109
QY 61 AAGAGAGAATTTTCCCAATTTGATATCTGATATATATTTTCTGGGGAGTCTTGGGAAAT 120
DB 110 AAGAGAGAATTTTCCCAATTTGATATCTGATATATATTTTCTGGGGAGTCTTGGGAAAT 169
QY 121 GGTTGTGCCATATATGTTTCTCGAGCCTTATAAGAAAGTCCACATCTGTGAACGTTTTTC 180
DB 170 GGTTGTGCCATATATGTTTCTCGAGCCTTATAAGAAAGTCCACATCTGTGAACGTTTTTC 229
QY 181 ATGCTTAATCTGGCCATTTCCAGATCTCTGTTTCAATAGCAGCTTCCCTTCAGGGCTGAC 240
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QY 241 TATTATCTTAGAGCTCCAAATTTGGATATTTTGGAGACCTGGCTTCAGGATTTATGCTTAT 300
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DB 350 TCCTTGTATGCAACATGTACAGCAGTATTTATTTCTGACCGTGTGAGTGTGTGCGT 409
QY 361 TTCTTGGCAATGGTTACCCCTTTCCGCTTCTGATGTCACGATCAGGAGTGCCTGG 420
DB 410 TTCTTGGCAATGGTTACCCCTTTCCGCTTCTGATGTCACGATCAGGAGTGCCTGG 469
QY 421 ATCTCTGTGGGATCATATGGATCTTATCATGGCTTCTCAATAATGCTCCTGGACAGT 480
DB 470 ATCTCTGTGGGATCATATGGATCTTATCATGGCTTCTCAATAATGCTCCTGGACAGT 529
QY 481 GGCTCTGAGCAGAACCGCAGTGTACATCATGCTTAGAGCTGAATCTCTATAAAATTTGCT 540
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 QY 600 ACTCAGCATCTGTTATCTGCTGATCAATTCGGGTTCTGTTAAA-AGTGGAGGTCACAGAAAT 658
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 Db 710 CGGGGCTGGGGTTTCTCACAGAAAG 736

RESULT 5
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 ACCESSION CD630089
 VERSION CD630089.1 GI:40278355
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 726)
 AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
 TITLE Circular rapid amplification of cDNA ends for high-throughput
 extension cloning of partial genes
 JOURNAL Genomics 84 (1), 205-210 (2004)
 COMMENT Contact: Fu GK
 Incyte Genomics, Inc.
 3160 Porter Dr., Palo Alto, CA 94304, USA
 Tel: 6508454102
 Email: gfu@incyte.com.

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 Best Local Similarity 99.4%; Pred. No. 5.6e-181;
 Matches 674; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 ATGGAAACCAATGGCACCTTCAGCAATAACAACAGCAGGAACCTGCACAATTGAAACTTC 60
 Db 50 ATGGAAACCAATGGCACCTTCAGCAATAACAACAGCAGGAACCTGCACAATTGAAACTTC 109
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 Db 110 AAGAGAGAATTTTCCCAATTGTATATCTGATAATATTTTCTGGGGAGCTTTGGGAAT 169
 QY 121 GGGTTGTCATATATGTTTTCTCGAGCCTTATAGAAGTCCACATCTCTGAACGTTTTC 180
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 QY 181 ATGCTAAATCTGGCCATTTTCAGATCTCTCTGTTTCAATAGCAGCGTTCCTTCAGGGCTGAC 240
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 QY 421 ATCTCTGTGGGATCATATGGATCTCTTATCATGGCTTCTCTCAATAATGTCTCTGGACAGT 480
 Db 470 ATCTCTGTGGGATCATATGGATCTCTTATCATGGCTTCTCTCAATAATGTCTCTGGACAGT 529
 QY 481 GGCTCTGACAGAAACGGCAGTGTGCATCATGCTTTAGAGTGAATCTCTATAAAATTTGCT 540
 Db 530 GGCTCTGACAGAAACGGCAGTGTGCATCATGCTTTAGAGTGAATCTCTATAAAATTTGCT 589
 QY 541 AAGCTGCAGACCACTAATATTCGCTTGGTGGTGGCTGCTGCTGCCATTTTTCACA 600
 Db 590 AAGCTGCAGACCACTAATATTCGCTTGGTGGTGGCTGCTGCTGCCATTTTTCACA 648
 QY 601 CTCAGCATCTGTTATCTGCTGATCAATTCGGGTTCTGTTAAAAGTGGAGGTCACAGAAATCG 660
 Db 649 CTCAGCATCTGTTATCTGCTGATCAATTCGGGTTCTGTTAAAAGTGGAGGTCACAGAAATCG 708
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 Db 709 GGGCTGGGGTTTCTCAC 726

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 LOCUS 56039988H1 FLP Homo sapiens cdna, mRNA sequence.
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 ACCESSION CD630075
 VERSION CD630075.1 GI:40278341
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 753)
 AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
 TITLE Circular rapid amplification of cDNA ends for high-throughput
 extension cloning of partial genes
 JOURNAL Genomics 84 (1), 205-210 (2004)
 COMMENT Contact: Fu GK
 Incyte Genomics, Inc.
 3160 Porter Dr., Palo Alto, CA 94304, USA
 Tel: 6508454102
 Email: gfu@incyte.com.

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 Matches 692; Conservative 0; Mismatches 5; Indels 7; Gaps 5;

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 Db 170 GGGTTGTCATATATGTTTTCTCGAGCCTTATAGAAGTCCACATCTCTGAACGTTTTC 229
 QY 181 ATGCTAAATCTGGCCATTTTCAGATCTCTCTGTTTCAATAGCAGCGTTCCTTCAGGGCTGAC 240
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Db 410 TTCTGCAATGGTTTCAACCTTTCCGCTTCTGATGTCACACATCAGGAGTGCCTGG 469
Qy 421 ATCTCTGTGGGATCATATGGATCCTTATCATGGCTTCTCTCAATAATGCTCCTGGACAGT 480
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Qy 481 GGCTCTGAGCAGAACGGCAGTGTACATCATGCTTAGAGCTGAATCTCTA-TAAAAATGC 539
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Qy 540 TAAGCTGACAGACCATGAATATTTGCTTGGTGGTGGCTGCTGCTGCCA-TTTTTCA 598
Db 590 TAAGCTGACAGACCATGAATATTTGCTTGGTGGTGGCTGCTGCTGCCA-TTTTTCA 649
Qy 599 CACTCAGCATCTGTTATCTG-CTGATCATTTGGGTTCTGTTAAAGTGGAGGTCCACAGAA 657
Db 650 CACTCAGCATCTGTTATCTGCTGATCATTTGGGTTCTGTTAAAGTGGAGGTCCACAGAA 708
Qy 658 TCGGGGCTGGGGTTTCCCTCACCAGGAAGCACTGACCAACAT 698
Db 709 TCGGGGCTGGGGTTTCCCTCACCAGGAAGCACTGACCAACAT 752

RESULT 7
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DEFINITION CD630077
ACCESSION CD630077
VERSION CD630077.1 GI:40278343
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 750)
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
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/db_xref="taxon:9606"
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Matches 683; Conservative 0; Mismatches 13; Indels 6; Gaps 5;

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Db 50 ATGGAACCAATGGCACCCTTCAGCAATAACACAGCAGGAATGCACAAATTTGAAACTTC 109
Qy 61 AAGAGAGAATTTTTCCCAATTGTATATCTGATAATAATTTTTCTGGGGAGTCTTTGGGAAT 120
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Db 170 GGGTTGTCATATATGTTTCCCTGCAGCCTTATAAGAGTCCACATCTGTGAAGCTTTTC 229
Qy 181 ATGCTAAATCTGGCCATTTCCAGATCTCTGTTTCAAGACGCTTCCCTTCAGGGCTGAC 240
Db 230 ATGCTAAATCTGGCCATTTCCAGATCTCTGTTTCAAGACGCTTCCCTTCAGGGCTGAC 289
Qy 241 TATTATCTTAGAGCTCCAAATTGGATATTTGGAGACCTGGCTCGCAGGATTTATGCTTTAT 300
Db 290 TATTATCTTAGAGCTCCAAATTGGATATTTGGAGACCTGGCTCGCAGGATTTATGCTTTAT 349
Qy 301 TCCTTGATGTCAACATGTACAGCAGTATTTATTTCTGACCGTGTGAGTGTGCGGT 360
Db 350 TCCTTGATGTCAACATGTACAGCAGTATTTATTTCTGACCGTGTGAGTGTGCGGT 409
Qy 361 TTCTGCAATGGTTTCAACCTTTCCGCTTCTGATGTCACACATCAGGAGTGCCTGG 420
Db 410 TTCTGCAATGGTTTCAACCTTTCCGCTTCTGATGTCACACATCAGGAGTGCCTGG 469
Qy 421 ATCTCTGTGGGATCATATGGATCCTTATCATGGCTTCTCTCAATAATGCTCCTGGACAGT 480
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Qy 540 T-AAGCTGACAGACCATGAATATTTGCTTGGTGGTGGCTGCTGCTGCCATTTTTC 598
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Db 649 AACTCAGCATCTGTTATCTGCTGATCCTCGGTTCTGTTAAAGTGGAGGTCCACAGAA 708
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Db 709 TCGGGGCTGGGGTTTCTCACCAGGAAGCACTGAAACACCA 750

RESULT 8
CD630069 673 bp mRNA linear EST 12-JAN-2004
LOCUS 56039916H1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD630069
ACCESSION CD630069
VERSION CD630069.1 GI:40278335
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 673)
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
1. .673
/organism="Homo sapiens"
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/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

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Query Match 62.48; Score 619.2; DB 6; Length 750;
Best Local Similarity 97.33; Pred. No. 9.8e-169;
Matches 683; Conservative 0; Mismatches 13; Indels 6; Gaps 5;

Qy 1 ATGGAACCAATGGCACCCTTCAGCAATAACACAGCAGGAATGCACAAATTTGAAACTTC 60
Db 50 ATGGAACCAATGGCACCCTTCAGCAATAACACAGCAGGAATGCACAAATTTGAAACTTC 109
Qy 61 AAGAGAGAATTTTTCCCAATTGTATATCTGATAATAATTTTTCTGGGGAGTCTTTGGGAAT 120
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Query Match      62.2%; Score 618; DB 6; Length 673;
Best Local Similarity 100.0%; Pred. No. 2.1e-168; Mismatches 0; Indels 0; Gaps 0;
Matches 618; Conservative 0;

QY 1 ATGGAACCAATGGCACTTCAGCAATAACAAACAGCAGGAAGTGCACAATTTGAAAATCTTC 60
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QY 61 AGAGAGAGATTTTCCCAATTTGATATCTGATATATTTTCTGGGGAGTCTTGGGAAT 120
DB 110 AGAGAGAGATTTTCCCAATTTGATATCTGATATATTTTCTGGGGAGTCTTGGGAAT 169
QY 121 GGGTTCTGCATATATGTTTTCTCGAGCCTTATAAGAGTCCACATCTGTGAACGTTTTTC 180
DB 170 GGGTTCTGCATATATGTTTTCTCGAGCCTTATAAGAGTCCACATCTGTGAACGTTTTTC 229
QY 181 ATGCTAAATCTGGCCATTTTCAGATCTCTGTTTCTAATAGCAGCGTTCCTTCAGGGCTGAC 240
DB 230 ATGCTAAATCTGGCCATTTTCAGATCTCTGTTTCTAATAGCAGCGTTCCTTCAGGGCTGAC 289
QY 241 TATTATCTTAGAGGCTCCCAATTTGGATATTTGGAGACCTGGCCTGCAGGATTTATGCTTAT 300
DB 290 TATTATCTTAGAGGCTCCCAATTTGGATATTTGGAGACCTGGCCTGCAGGATTTATGCTTAT 349
QY 301 TCCTTGATGTCAACATGTACAGCAGTATTTATTTCTGACCGTCTGAGTGTGTGCGT 360
DB 350 TCCTTGATGTCAACATGTACAGCAGTATTTATTTCTGACCGTCTGAGTGTGTGCGT 409
QY 361 TTCTCTGGCAATGGTTTCAACCCCTTTCCGCTTCTGCAATGTCCACAGATCAGGAGTGCCTGG 420
DB 410 TTCTCTGGCAATGGTTTCAACCCCTTTCCGCTTCTGCAATGTCCACAGATCAGGAGTGCCTGG 469
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DB 470 ATCTCTGTGGGATCATATGGATTCCTTATTCATGGCTTCTCAATATGCTCTCTGGAAGT 529
QY 481 GGCTCTGAGCAGAACGGCAGTGTGCATCATCTTAGAGTCAATCTCTATATAAATTTGCT 540
DB 530 GGCTCTGAGCAGAACGGCAGTGTGCATCATCTTAGAGTCAATCTCTATATAAATTTGCT 589
QY 541 AAGCTGCAGACCATGAATCAATATTTGCTTTGGTGGGCTGCTGCTGCATTTTTCACA 600
DB 590 AAGCTGCAGACCATGAATCAATATTTGCTTTGGTGGGCTGCTGCTGCATTTTTCACA 648
QY 601 CTCAGCATCTGTATCTGCTGATCATTTGGGTTCTGTTAAAGTGGAGGTCACAGATCG 660
DB 650 CTCAGCATCTGTATCTG 667

RESULT 9
LOCUS C0959148
DEFINITION AGENCOURT_30842618 NIH_MGC_146 Homo sapiens cDNA clone
IMAGE:7389737 5', mRNA sequence.
ACCESSION C0959148
VERSION C0959148.1 GI:51323730
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 729)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: ggapbs-r@mail.nih.gov
Tissue Procurement: Guthrie cDNA Resource Center
cdna Library Preparation: Guthrie cDNA Resource Center
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cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBI7 row: f column: 03
High quality sequence stop: 602.
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        1..729
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multiple; ORF's were PCR-amplified (from IMAGE Clones or
from commercially available cDNA libraries) and cloned by
the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)
into pcDNA3.1. For specific information on cloning sites
(which vary by clone), please refer to the Guthrie
website, using the Guthrie ID given in the file
ftp://image.llnl.gov/image.rearrayed_plates/IRBF.presv.dat
a. Note: this is a NIH_MGC Library."
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ORIGIN

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Query Match      61.1%; Score 607.2; DB 7; Length 729;
Best Local Similarity 94.7%; Pred. No. 3e-165;
Matches 648; Conservative 0; Mismatches 32; Indels 4; Gaps 2;

QY 1 ATGGAACCAATGGCACTTCAGCAATAACAAACAGCAGGAAGTGCACAATTTGAAAATCTTC 60
DB 50 ATGGAACCAATGGCACTTCAGCAATAACAAACAGCAGGAAGTGCACAATTTGAAAATCTTC 109
QY 61 AGAGAGAGATTTTCCCAATTTGATATCTGATATATTTTCTGGGGAGTCTTGGGAAT 120
DB 110 AGAGAGAGATTTTCCCAATTTGATATCTGATATATTTTCTGGGGAGTCTTGGGAAT 169
QY 121 GGGTTCTGCATATATGTTTTCTCGAGCCTTATAAGAGTCCACATCTCTGACCGTTTTTC 180
DB 170 GGGTTCTGCATATATGTTTTCTCGAGCCTTATAAGAGTCCACATCTCTGACCGTTTTTC 229
QY 181 ATGCTAAATCTGGCCATTTTCAGATCTCTGTTTCTAATAGCAGCGTTCCTTCAGGGCTGAC 240
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QY 241 TATTATCTTAGAGGCTCCCAATTTGGATATTTGGAGACCTGGCCTGCAGGATTTATGCTTAT 300
DB 290 TATTATCTTAGAGGCTCCCAATTTGGATATTTGGAGACCTGGCCTGCAGGATTTATGCTTAT 349
QY 301 TCCTTGATGTCAACATGTACAGCAGTATTTATTTCTGACCGTCTGAGTGTGTGCGT 360
DB 350 TCCTTGATGTCAACATGTACAGCAGTATTTATTTCTGACCGTCTGAGTGTGTGCGT 409
QY 361 TTCTCTGGCAATGGTTTCAACCCCTTTCCGCTTCTGCAATGTCCACAGATCAGGAGTGCCTGG 420
DB 410 TTCTCTGGCAATGGTTTCAACCCCTTTCCGCTTCTGCAATGTCCACAGATCAGGAGTGCCTGG 469
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DB 470 ATCTCTGTGGGATCATATGGATTCCTTATTCATGGCTTCTCAATATGCTCTCTGGAAGT 529
QY 481 GGCTCTGAGCAGAACGGCAGTGTGCATCATCTTAGAGTCAATCTCTATATAAATTTGCT 540
DB 530 GGCTCTGAGCAGAACGGCAGTGTGCATCATCTTAGAGTCAATCTCTATATAAATTTGCT 589
QY 541 AAGCTGCAGACCATGAATCAATATTTGCTTTGGTGGGCTGCTGCTGCATTTTTCACA 600
DB 590 AAGCTGCAGACCATGAATCAATATTTGCTTTGGTGGGCTGCTGCTGCATTTTTCACA 648
QY 601 CTCAGCATCTGTATCTGCTGATCATTTGGGTTCTGTTAAAGTGGAGGTCACAGATCG 660
DB 650 CTCAGCATCTGTATCTG 667
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Db      649 CTCAGCATCTGTATCTGCTGATCATTCCTCGGTTCTTTAAATAATTGAAG---TCNGAATC 705
Qy      661 GGCTCGGGGTTTCTCACAGGAAG 684
Db      706 NNGCTCGGGGTTTTCACAAAGAAAG 729

RESULT 10
LOCUS   CD630079             652 bp      mRNA      linear      EST 12-JAN-2004
DEFINITION 5604008H1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION  CD630079
VERSION    CD630079.1 GI:40278345
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE     1 (bases 1 to 652)
          Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
          Circular rapid amplification of cDNA ends for high-throughput
          extension cloning of partial genes
JOURNAL   Genomics 84 (1), 205-210 (2004)
COMMENT   Contact: Fu GK
          Incyte Genomics, Inc.
          3160 Porter Dr., Palo Alto, CA 94304, USA
          Tel: 6508454102
          Email: gfu@incyte.com.

FEATURES             source
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Query Match      60.7%; Score 603; DB 6; Length 652;
Best Local Similarity 100.0%; Pred. No. 4.9e-164;
Matches 603; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  ATGGAACCAATGGCACCTTCAGCAATAACACAGCAGGAAGTCGACAAATTGAAAATTC 60
Db      50  ATGGAACCAATGGCACCTTCAGCAATAACACAGCAGGAAGTCGACAAATTGAAAATTC 109
Qy      61  AAGAGAGAAATTTTCCCAATGTATATCTGATATATTTTCTGGGAGTCTTGGGAAT 120
Db      110  AAGAGAGAAATTTTCCCAATGTATATCTGATATATTTTCTGGGAGTCTTGGGAAT 169
Qy      121  GGGTTGTCCATATATGTTTCTCGAGCCTTATAAGAAAGTCCACATCTGTGAACGTTTTC 180
Db      170  GGGTTGTCCATATATGTTTCTCGAGCCTTATAAGAAAGTCCACATCTGTGAACGTTTTC 229
Qy      181  ATGCTAAATCTGGCCATTTCAGATCTCTGTTTCCATAGAGCGTCTCCCTTCAGGGCTGAC 240
Db      230  ATGCTAAATCTGGCCATTTCAGATCTCTGTTTCCATAGAGCGTCTCCCTTCAGGGCTGAC 289
Qy      241  TATTATCTTAGAGCTCCAAATTTGATATTTGGAGACCTGGCCTGCAGGATTATGCTTAT 300
Db      290  TATTATCTTAGAGCTCCAAATTTGATATTTGGAGACCTGGCCTGCAGGATTATGCTTAT 349
Qy      301  TCCTTGTATGTCAACATGTACAGCAGTATTTATTTCTGACCGTGTGAGTGTGTGCGT 360
Db      350  TCCTTGTATGTCAACATGTACAGCAGTATTTATTTCTGACCGTGTGAGTGTGTGCGT 409
Qy      361  TTCTTGCAATGGTTTCAACCGTCTTCGATGTCAACAGCATCAGAGTGCCTGG 420
Db      410  TTCTTGCAATGGTTTCAACCGTCTTCGATGTCAACAGCATCAGAGTGCCTGG 469
Qy      421  ATCCTCTGTGGATCATATGATCCTTATCATGCGTTCCTCAATAATGCTCCTGGACAT 480
Db      470  ATCCTCTGTGGATCATATGATCCTTATCATGCGTTCCTCAATAATGCTCCTGGACAT 529
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Qy      481  GGCCTCTGAGCAGAACGGCAGTGTCAATCATGCTTAGAGCTGAATCTCTATAAAATTCCT 540
Db      530  GGCTCTGAGCAGAACGGCAGTGTCAATCATGCTTAGAGCTGAATCTCTATAAAATTCCT 589
Qy      541  AAGCTCGACACCAATGAACCTATATTTGCTTGGTGGCTGCTGCTGCCATTTTTCACA 600
Db      590  AAGCTCGACACCAATGAACCTATATTTGCTTGGTGGTGGCTGCTGCCATTTTTCACA 649
Qy      601  CTC 603
Db      650  CTC 652

RESULT 11
LOCUS   CD630087             670 bp      mRNA      linear      EST 12-JAN-2004
DEFINITION 5604008H1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION  CD630087
VERSION    CD630087.1 GI:40278353
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE     1 (bases 1 to 670)
          Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
          Circular rapid amplification of cDNA ends for high-throughput
          extension cloning of partial genes
JOURNAL   Genomics 84 (1), 205-210 (2004)
COMMENT   Contact: Fu GK
          Incyte Genomics, Inc.
          3160 Porter Dr., Palo Alto, CA 94304, USA
          Tel: 6508454102
          Email: gfu@incyte.com.

FEATURES             source
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     /note="Vector: pDrive Cloning Vector"

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Query Match      60.4%; Score 599.4; DB 6; Length 670;
Best Local Similarity 99.7%; Pred. No. 5.5e-163;
Matches 611; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy      1  ATGGAACCAATGGCACCTTCAGCAATAACACAGCAGGAAGTCGACAAATTGAAAATTC 60
Db      50  ATGGAACCAATGGCACCTTCAGCAATAACACAGCAGGAAGTCGACAAATTGAAAATTC 109
Qy      61  AAGAGAGAAATTTTCCCAATGTATATCTGATATATTTTCTGGGAGTCTTGGGAAT 120
Db      110  AAGAGAGAAATTTTCCCAATGTATATCTGATATATTTTCTGGGAGTCTTGGGAAT 169
Qy      121  GGGTTGTCCATATATGTTTCTCGAGCCTTATAAGAAAGTCCACATCTGTGAACGTTTTC 180
Db      170  GGGTTGTCCATATATGTTTCTCGAGCCTTATAAGAAAGTCCACATCTGTGAACGTTTTC 229
Qy      181  ATGCTAAATCTGGCCATTTCAGATCTCTGTTTCCATAGAGCGTCTCCCTTCAGGGCTGAC 240
Db      230  ATGCTAAATCTGGCCATTTCAGATCTCTGTTTCCATAGAGCGTCTCCCTTCAGGGCTGAC 289
Qy      241  TATTATCTTAGAGCTCCAAATTTGATATTTGGAGACCTGGCCTGCAGGATTATGCTTAT 300
Db      290  TATTATCTTAGAGCTCCAAATTTGATATTTGGAGACCTGGCCTGCAGGATTATGCTTAT 349
Qy      301  TCCTTGTATGTCAACATGTACAGCAGTATTTATTTCTGACCGTGTGAGTGTGTGCGT 360
Db      350  TCCTTGTATGTCAACATGTACAGCAGTATTTATTTCTGACCGTGTGAGTGTGTGCGT 409
Qy      361  TTCTTGCAATGGTTTCAACCGTCTTCGATGTCAACAGCATCAGAGTGCCTGG 420
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Db      410  TTCTGGCAATGGTTACCCCTTTCCGCTTCTGCTGCTCACCAGCATCAGGAGTGCCTGG 469
Qy      421  ATCTCTGTGGGATCATATGGATCCTTATCATGCTTCTCCTCAATAATGCTCCTGGACAGT 480
Db      470  ATCTCTGTGGGATCATATGGATCCTTATCATGCTTCTCCTCAATAATGCTCCTGGACAGT 529
Qy      481  GGCTCTGAGCAGAACGGCAGTGTACATCATGCTTTAGAGCTGAATCTCTATAAAATTGCT 540
Db      530  GGCTCTGAGCAGAACGGCAGTGTACATCATGCTTTAGAGCTGAATCTCTATAAAATTGCT 589
Qy      541  AAGCTGCAGACCAATGAACATATATGCTTGGTGGTGGCTGCTGCCATTTTTCACA 600
Db      590  AAGCTGCAGACCAATGAACATATATGCTTGGTGGTGGCTGCTGCCATTTTTCACA 648
Qy      601  CTCAGCATCTGTT 613
Db      649  CTCAGCATCTGTT 661

RESULT 12
CD630081
LOCUS      CD630081                663 bp      mRNA      linear      EST 12-JAN-2004
DEFINITION 56040016H1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION  CD630081
VERSION    CD630081.1 GI:40278347
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE  1 (bases 1 to 663)
AUTHORS    Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE      Circular rapid amplification of cDNA ends for high-throughput
            extension cloning of partial genes
JOURNAL    Genomics 84 (1), 205-210 (2004)
COMMENT    Contact: Fu GK
            Incyte Genomics, Inc.
            3160 Porter Dr., Palo Alto, CA 94304, USA
            Tel: 6508454102
            Email: gfu@incyte.com.

FEATURES   source
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Query Match      60.1%; Score 596.8; DB 6; Length 663;
Best Local Similarity 99.3%; Pred. No. 3.2e-162;
Matches 610; Conservative 0; Mismatches 12; Indels 2; Gaps 1;

Qy      1  ATGGAACCAAAATGGCACTTCAGCAATAACAACAGCAGGAAGTCACAAATTGAAAACCTTC 60
Db      50  ATGGAACCAAAATGGCACTTCAGCAATAACAACAGCAGGAAGTCACAAATTGAAAACCTTC 109
Qy      61  AAGAGAGAAATTTTCCCAATTTGATATCTGATATATATTTTCTGGGGAGCTCTGGGAAT 120
Db      110  AAGAGAGAAATTTTCCCAATTTGATATCTGATATATATTTTCTGGGGAGCTCTGGGAAT 169
Qy      121  GGGTTCTCCATATATGTTTTCTCGAGCCTTATAAGAAGTCACATCTGTGAACGTTTTTC 180
Db      170  GGGTTCTCCATATATGTTTTCTCGAGCCTTATAAGAAGTCACATCTGTGAACGTTTTTC 229
Qy      181  ATGCTAAATCTGGCCATTTTCAGATCTCCTGTTTATGAAGCAGCGTTCCCTTCAGGGCTGAC 240
Db      230  ATGCTAAATCTGGCCATTTTCAGATCTCCTGTTTATGAAGCAGCGTTCCCTTCAGGGCTGAC 289
Qy      241  TATTATCTTAGAGGCTCCCAATTGGATATTTGGAGACCTGGCCTGCGAGGATTATGCTTAT 300
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Qy      301  TCCTTGATGTCAACATGTACAGCAGTATTTATTTCTCAGCCGTGCTGAGTGTGTGCGT 360
Db      350  TCCTTGATGTCAACATGTACAGCAGTATTTATTTCTGACCGTGTGAGTGTGTGCGT 409
Qy      361  TTCCTGGCAATGGTTACCCCTTTCCGCTTCTGCAATGTCACCAGCATCAGGAGTGCCTGG 420
Db      410  TTCCTGGCAATGGTTACCCCTTTCCGCTTCTGCAATGTCACCAGCATCAGGAGTGCCTGG 469
Qy      421  ATCTCTGTGGGATCATATGGATCCTTATCATGCTTCTCCTCAATAATGCTCCTGGACAGT 480
Db      470  ATCTCTGTGGGATCATATGGATCCTTATCATGCTTCTCCTCAATAATGCTCCTGGACAGT 529
Qy      481  GGCTCTGAGCAGAACGGCAGTGTACATCATGCTTTAGAGCTGAATCTCTATAAAATTGCT 540
Db      530  GGCTCTGAGCAGAACGGCAGTGTACATCATGCTTTAGAGCTGAATCTCTATAAAATTGCT 589
Qy      541  AAGCTGCAGACCAATGAACATATATGCTTGGTGGTGGCTGCTGCCATTTTTCACA 598
Db      590  AAGCTGCAGACCAATGAACATATATGCTTGGTGGTGGCTGCTGCCATTTTTCACA 649
Qy      599  CACTCAGCATCTGTT 612
Db      650  CACTCAGCATCTGTT 663

RESULT 13
CD630067
LOCUS      CD630067                682 bp      mRNA      linear      EST 12-JAN-2004
DEFINITION 56039908H1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION  CD630067
VERSION    CD630067.1 GI:40278333
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE  1 (bases 1 to 682)
AUTHORS    Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE      Circular rapid amplification of cDNA ends for high-throughput
            extension cloning of partial genes
JOURNAL    Genomics 84 (1), 205-210 (2004)
COMMENT    Contact: Fu GK
            Incyte Genomics, Inc.
            3160 Porter Dr., Palo Alto, CA 94304, USA
            Tel: 6508454102
            Email: gfu@incyte.com.

FEATURES   source
            Location/Qualifiers
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ORIGIN
Query Match      59.8%; Score 593.4; DB 6; Length 682;
Best Local Similarity 97.2%; Pred. No. 3.1e-161;
Matches 615; Conservative 0; Mismatches 16; Indels 2; Gaps 1;

Qy      1  ATGGAACCAAAATGGCACTTCAGCAATAACAACAGCAGGAAGTCACAAATTGAAAACCTTC 60
Db      50  ATGGAACCAAAATGGCACTTCAGCAATAACAACAGCAGGAAGTCACAAATTGAAAACCTTC 109
Qy      61  AAGAGAGAAATTTTCCCAATTTGATATCTGATATATATTTTCTGGGGAGCTCTGGGAAT 120
Db      110  AAGAGAGAAATTTTCCCAATTTGATATCTGATATATATTTTCTGGGGAGCTCTGGGAAT 169
Qy      121  GGGTTCTCCATATATGTTTTCTCGAGCCTTATAAGAAGTCACATCTGTGAACGTTTTTC 180
Db      170  GGGTTCTCCATATATGTTTTCTCGAGCCTTATAAGAAGTCACATCTGTGAACGTTTTTC 229
Qy      181  ATGCTAAATCTGGCCATTTTCAGATCTCCTGTTTATGAAGCAGCGTTCCCTTCAGGGCTGAC 240

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Db 230 ATGCTAAATCGGCCATTTCAGATCTCCTGTTTCATAGACGCTTCCCTTCAGGGCTGAC 289
Qy 241 TATTATCTTAGAGGCTCCAAATTTGGATATTTGGAGACCTGGCCCTGCAGGATTATGCTTTAT 300
Db 290 TATTATCTTAGAGGCTCCAAATTTGGATATTTGGAGACCTGGCCCTGCAGGATTATGCTTTAT 349
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Db 350 TCCTTGATGTCACATGTAACAGTACAGAGTATTTATTTCTGACCGTGCTGAGTGTGTGCGT 409
Qy 361 TTCTTGCAATGTTTACCCCTTTCGGCTTCTGATGTCATGTCACAGCATCAGAGTGTGCTGG 420
Db 410 TTCTTGCAATGTTTACCCCTTTCGGCTTCTGATGTCACAGCATCAGAGTGTGCTGG 469
Qy 421 ATCTCTGTGGGATCATATGATGCTTTCATGATGCTTTCCTCAATATGCTTCCTGGACAGT 480
Db 470 ATCTCTGTGGGATCATATGATGCTTTCATGATGCTTTCCTCAATATGCTTCCTGGACAGT 529
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Qy 539 CTAAGCTGACAGCAGTGAATATTTGCTTGGCTTGGTGGCTGCTGCTGCCATTTTCA 598
Db 590 CTAAGCTGACAGCAGTGAATATTTGCTTGGCTTGGTGGCTGCTGCTGCCATTTTTCAC 649
Qy 599 CACTCAGCATCTGTTATCTGCTGATCATTCGGG 631
Db 650 ACCTCAGCATCTGTTATCTGCTGATCATTCGGG 682

RESULT 14
CF147785
LOCUS
DEFINITION
AGENCOURT 14740183 NIH MGC_145 Homo sapiens cDNA clone
IMAGE:6971946 5', mRNA sequence.
CF147785
VERSION
KEYWORDS
SOURCE
Homo sapiens (human)
Homo sapiens
REFERENCE
NIH-MGC http://mgi.nci.nih.gov/
1 (bases 1 to 729)
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
COMMENT
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabs-x@mail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: INB102 row: f column: 05
High quality sequence stop: 659.
Location/Qualifiers
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/note="vector: pCDNA3.1; Site 1: varies by clone; Site 2:
varies by clone; ORFs were PCR-amplified and cloned into
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by

clone and include the following: 5'-EcoRV-XmnI/XhoI-3',
5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).
For information about which gene each clones represents,
please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBI.presv.dat
a Note: this is a NIH_MGC Library."

Query Match 56.9%; Score 565; DB 7; Length 729;
Best Local Similarity 100.0%; Pred. No. 66-153;
Matches 565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS
DEFINITION
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ACCESSION
CD630066.1 GI:40278332
VERSION
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 633)
AUTHORS
Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
TITLE
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL
Genomics 84 (1), 205-210 (2004)
COMMENT
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102

CD630066 633 bp mRNA linear EST 12-JAN-2004
56039816R6 FLP Homo sapiens cDNA, mRNA sequence.
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Homo sapiens (human)
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1 (bases 1 to 633)
Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102

Email: gfu@incyte.com.

FEATURES

Location/Qualifiers
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Job time : 3259 secs


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RESULT 2
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DEFINITION Novel polypeptide.
ACCESSION BD131273
VERSION BD131273.1 GI:23226218
KEYWORDS JP 2002017378-A/1.
SOURCE Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Lee, H.
Novel polypeptide
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PFIZER INC
TITLE
JOURNAL
COMMENT OS Homo sapiens (human)
PN JP 2002017378-A/1
PD 22-JAN-2002
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PR 05-APR-2000 GB 0008504.3
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LOCUS
DEFINITION Homo sapiens gene for cysteinyl leukotriene receptor like receptor.
ACCESSION AB041644
VERSION AB041644.1 GI:10716135
KEYWORDS cysteinyl leukotriene receptor like receptor.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 993)
AUTHORS Suga,H.
TITLE Homo sapiens cysteinyl leukotriene receptor 1 like receptor
JOURNAL Published Only in DataBase (2000)
REFERENCE 2 (bases 1 to 993)
AUTHORS Suga,H.
TITLE Direct Submission
JOURNAL Submitted (10-APR-2000) Hinako Suga, Faculty of Medicine,
University of Tokyo, Department of Neurochemistry; 7-3-1, Hongo,
Tokyo 113-0033, Japan (E-mail:hsuga@n.u-tokyo.ac.jp,
Tel:81-3-5841-3560, Fax:81-3-3814-8154)

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CDS

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.9e-286;
Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4
AX644576
LOCUS
DEFINITION Sequence 54 from Patent WO02086123.
ACCESSION AX644576
VERSION AX644576.1 GI:28610619

AX644576 1026 bp DNA linear PAT 27-FEB-2003

KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
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REFERENCE	1
AUTHORS	Feder, J., Nelson, T. C., Ramanathan, C., Cacace, A. M. and Barber, L. E.
TITLE	A novel human g-protein coupled receptor hgrpmyl1 expressed highly in heart and variants thereof
JOURNAL	Patent: WO 02086123-A 54 31-OCT-2002;
FEATURES	Bristol-Myers Squibb Co. (US)
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Best Local Similarity	100.0%; Pred. No. 3e-286;
Matches 993; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS	Novel G-protein coupled receptors. 1041 bp DNA linear PAT 17-JAN-2003
DEFINITION	BD144304
ACCESSION	BD144304.1 GI:27850062
VERSION	JP 2002112793-A/29.
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 1041)
AUTHORS	Haga, T., Takeda, S. and Miyake, N.
TITLE	Novel G-protein coupled receptors
JOURNAL	Patent: JP 2002112793-A 29 16-APR-2002;
	JAPAN SCIENCE AND TECHNOLOGY CORP
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	PC C12N15/09, A01K67/027, A61K38/00, A61K39/395, A61K39/395, A61K45/00, PC
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	C12N1/21,
	PC C12N5/10, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/53, PC
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	PC C12P21/08, C12N15/00, A61K37/02, C12N5/00
	CC Novel G-protein coupled receptors
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Query Match	100.0%; Score 993; DB 6; Length 1041;
Best Local Similarity	100.0%; Pred. No. 3e-286;
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RESULT 6
Q0739544
LOCUS
DEFINITION Sequence 25478 from Patent WO02068579.
linear PAT 03-FEB-2004

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ACCESSION Q0739544
VERSION Q0739544.1 GI:42342834
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof
JOURNAL Patent: WO 02068579-A 25478 06-SEP-2002;
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source PG Corporation (NY) (US)
location/Qualifiers
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Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 7
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LOCUS
DEFINITION
Sequence 13 from Patent WO0136471.
ACCESSION
AX148172
VERSION
AX148172.1 GI:14347079
KEYWORDS
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SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Chen,R., Dang,H.T. and Lowitz,K.P.
AUTHORS
Endogenous and non-endogenous versions of human g protein-coupled
TITLE
receptors
JOURNAL
Patent: WO 0136471-A 13 25-MAY-2001;
Arena Pharmaceuticals, Inc. (US)
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LOCUS
DEFINITION
Sequence 1 from Patent WO0168842.
ACCESSION
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VERSION
AX252467.1 GI:15985746
KEYWORDS
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SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Xiao,Y.
AUTHORS
Regulation of human p2y-like gpcr protein
TITLE
Patent: WO 0168842-A 1 20-SEP-2001;
Bayer Aktiengesellschaft (DE)
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LOCUS AX281256 1041 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 1 from Patent WO0177149.
ACCESSION AX281256

VERSION AX281256.1 GI:16608512
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
- ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Xiao, Y.
TITLE Regulation of human cyslt2-like gper protein
JOURNAL Patent: WO 0177149-A 1 18-OCT-2001;
Bayer Aktiengesellschaft (DE)
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Db 1009 AGTGTGCTGTTGAGAAAGGAAACAAGAGTATAA 1041

RESULT 10
AX304816
LOCUS AX304816 1041 bp DNA linear PAT 11-DEC-2001
DEFINITION Sequence 5 from Patent EP1158050.
ACCESSION AX304816
VERSION AX304816.1 GI:17644495
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Harland, L.
AUTHORS Human cysteinyl leukotriene receptor (cyslt2)
TITLE Patent: EP 1158050-A 5 28-NOV-2001;
JOURNAL Pfizer Limited (GB); PFIZER INC. (US)
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Query Match 100.0%; Score 993; DB 6; Length 1041;
Best Local Similarity 100.0%; Pred. No. 3e-286;
Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 901 AAGTCTGCACTCAGAAAGGCCATCCACAGAGGCAAAAGCAAAAGTGTGTTTCCCTGTT 960
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Db 1009 AGTGTGCTGTTGAGAAAGGAAACAAGAGTATAA 1041

RESULT 11
AX417072
LOCUS AX417072 1041 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 6 from Patent WO0192302.
ACCESSION AX417072
VERSION AX417072.1 GI:21449674
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Murphy, P. and Martin, J.
AUTHORS Novel nucleic acids, polypeptides, methods of making, and uses
TITLE thereof
JOURNAL Patent: WO 0192302-A 6 06-DEC-2001;
FEATURES REGENERON PHARMACEUTICALS, INC. (US)
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Db	109	AAGAGAGAAATTTTCCCAATGATATCTGATAATATTTTCTGGGAGCTCTGGGAAAT	168
Qy	121	GGGTGTGCCATATATGTTTCTCGACGCTTATAAGAGTCCACATCTGTGAACGTTTTC	180
Db	169	GGGTGTGCCATATATGTTTCTCGACGCTTATAAGAGTCCACATCTGTGAACGTTTTC	228
Qy	181	ATGCTAAATCTGGCCATTTCCAGATCTCTGCTTATATAAGCAGCGCTTCCCTTCAGGCGTGAC	240
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Db	109	AAGAGAGAAATTTTCCCAATGATATCTGATAATATTTTCTGGGAGCTCTGGGAAAT	168
Qy	121	GGGTGTGCCATATATGTTTCTCGACGCTTATAAGAGTCCACATCTGTGAACGTTTTC	180
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Qy	181	ATGCTAAATCTGGCCATTTCCAGATCTCTGCTTATATAAGCAGCGCTTCCCTTCAGGCGTGAC	240
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Qy	241	TATTATCTTAGAGCTCCAAATGGATATTTGGAGACCTCGGCTCGAGGATATGCTTTAT	300
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Qy	301	TCCTTGTATGTCACATGTACAGCAGTATTTATTTCTGACCGTGCAGTGTGTGCGGT	360
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LOCUS		Sequence 29 from Patent WO02086123.	
DEFINITION		AX644551	
ACCESSION		AX644551	
VERSION		AX644551.1 GI:28610609	
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ORGANISM		Homo sapiens	
REFERENCE		1. Feder, J., Nelson, T. C., Ramanathan, C., Cacace, A. M. and Barber, L. E. A novel human g-protein coupled receptor hgrpmyl1 expressed highly in heart and variants thereof Patent: WO 02086123-A 29 31-Oct-2002; Bristol-Myers Squibb Co. (US) Location/Qualifiers 1. .1041 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" 1. .1041 /note="unnamed protein product"	
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TITLE		A novel human g-protein coupled receptor hgrpmyl1 expressed highly in heart and variants thereof	
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Qy	61	AAGAGAGAAATTTTCCCAATGATATCTGATAATATTTTCTGGGAGCTCTGGGAAAT	120
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Qy	121	GGGTGTGCCATATATGTTTCTCGACGCTTATAAGAGTCCACATCTGTGAACGTTTTC	180
Db	169	GGGTGTGCCATATATGTTTCTCGACGCTTATAAGAGTCCACATCTGTGAACGTTTTC	228
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RESULT 13

BD131276
LOCUS Novel polypeptide.
DEFINITION Novel polypeptide.
ACCESSION BD131276
VERSION BD131276.1 GI:23226221
KEYWORDS JP 2002017378-A/4.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE

Novel polypeptide
Patent: JP 2002017378-A 4 22-JAN-2002;
PFIZER INC

COMMENT

OS Homo sapiens (human)
PN JP 2002017378-A/4
PD 22-JAN-2002
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PR 05-APR-2000 GB 0008504.3

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PC A61P37/00,
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FEATURES
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Query Match 100.0%; Score 993; DB 6; Length 1041;
Best Local Similarity 100.0%; Pred. No. 3e-286;
Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGGAAACCAATGGCAACCTTCAGCAATAACAACAGCAGGAACCTGCACAAATTGAAAACTTC 60
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 Qy 961 AGTGTGTGGTTGAGAAAGGAAACAAGAGTATAA 993
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RESULT 14
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 DEFINITION Homo sapiens GPCR gene for putative G-protein coupled receptor,
 complete CDS, clone:hGPCR21.
 ACCESSION AB083603
 VERSION AB083603.1 GI:20152269
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Takeda,S., Kadowaki,S., Haga,T., Takaesu,H. and Mitaku,S.
 TITLE Identification of G protein-coupled receptor genes from the human
 genome sequence
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1041)
 AUTHORS Takeda,S., Kadowaki,S., Haga,T., Takaesu,H. and Mitaku,S.
 TITLE Direct Submission
 JOURNAL Submitted (10-APR-2002) Shigeki Takeda, Gunma University,
 Department of Biological and Chemical, Engineering, Faculty of
 Engineering; 1-5-1, Kiryu, Gunma 376-8515, Japan
 (E-mail:stakeda@bce.gunma-u.ac.jp, Tel:+81-277-30-1434,
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gene
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 Best Local Similarity 100.0%; Pred. No. 3e-286;
 Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

RESULT 15
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 DEFINITION Homo sapiens cysteinyl leukotriene receptor CYSUR2 gene, complete

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